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19/827

From: Whiteman, Brian
Sent: Thursday, November 10, 2005 10:35 AM
To: STIC-Biotech/ChemLib
Subject: seq search

10/696,282 Wilson et al.

SEQ ID NO: 13, 15, and 17 and

nucleotides 335 to 2272 of SEQ ID NO: 1 and nucleotides 1007 to 2272 of SEQ ID NO: 1:

- 1) search against us issued and published us patent database
- 2) commercial databases

thank you,

Brian Whiteman
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mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Searcher: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
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WWW/Internet: _____
Other (Specify): _____

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From: Whiteman, Brian
Sent: Thursday, November 10, 2005 10:41 AM
To: STIC-Biotech/ChemLib
Subject: seq search

10/696,900 Wilson et al.

nucleotides 1 to 143 of SEQ ID NO: 1; nucleotides 4576-4718 of SEQ ID NO: 1; nucleotides 2223-4431 of
SEQ ID NO: 1; **nucleotides 2829-4432** of SEQ ID NO: 1
1) search against us issued and published us patent database
2) commercial databases

thank you,

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Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

1-4718 NH

11/30/05
JH

Searcher: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Total time: _____
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Search Site
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Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 17:24:49 ; Search time 131.527 Seconds
(without alignment)
2458.679 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MAADGYLPDWMEDNLSEGR.....NNGLYTEPPPIGTRYLTRPL 736

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3989	100.0	736	3	AAV71167
2	3989	100.0	736	6	ABBB80232
3	3989	100.0	736	7	ABR62762
4	3989	100.0	736	7	ADZ76565
5	3989	100.0	736	9	ADV70294
6	3989	100.0	736	9	ADZ27069
7	3989	100.0	736	9	ADZ27012
8	3985	99.9	736	9	ADV67506
9	3968	99.5	736	4	ADZ27007
10	3963	99.3	736	4	AABS59847
11	3963	99.3	736	7	ADZ76566
12	3963	99.3	736	9	ADV70293
13	3963	99.3	736	9	ADZ27070
14	3987.5	97.7	737	9	ADZ27086
15	3983.5	97.4	737	9	ADZ27010
16	3983	97.3	736	9	ADZ27074
17	3873	97.1	736	9	ADZ27008
18	3853	96.6	736	9	ADZ27009
19	3511	88.0	736	4	AABS59846
20	3494	87.6	736	4	AABS59845
21	3494	87.6	736	6	ABBR0233
22	3494	87.6	736	7	ABR62763
23	3494	87.6	736	7	ADZ76572
24	3494	87.6	736	9	ADV67507

25	3494	87.6	736	9	ADZ27067	Adz27067 Adeno-sss
26	3483.5	87.3	737	9	ADZ26959	Adz26959 Adeno-sss
27	3476	87.1	736	9	ADZ27085	Adz27085 Adeno-sss
28	3473	87.1	736	7	ADZ76598	Adz76598 Adeno-sss
29	3469	87.0	738	9	ADZ26960	Adz26960 Adeno-sss
30	3467	86.9	736	6	ABBR0229	Abbr0229 AAV9 cap
31	3467	86.9	736	7	ABR62764	AbR62764 Adeno-sss
32	3467	86.9	736	7	ADZ76601	Adz76601 Adeno-sss
33	3467	86.9	736	7	ADZ76508	Adz76508 Amino aci
34	3464.5	86.9	737	9	ADZ27080	Adz27080 Adeno-sss
35	3464	86.8	736	7	ADZ76597	Adz76597 Adeno-sss
36	3460	86.7	736	7	ADZ76599	Adz76599 Adeno-sss
37	3458.5	86.7	737	9	ADZ26963	Adz26963 Adeno-sss
38	3457	86.7	736	7	ADZ76600	Adz76600 Adeno-sss
39	3456.5	86.7	735	9	ADZ27034	Adz27034 Adeno-sss
40	3456.5	86.7	737	9	ADZ26966	Adz26966 Adeno-sss
41	3456.5	86.7	737	9	ADZ26962	Adz26962 Adeno-sss
42	3456	86.6	738	9	ADZ26951	Adz26951 Adeno-sss
43	3455.5	86.6	737	9	ADZ26965	Adz26965 Adeno-sss
44	3453.5	86.6	735	9	ADZ26996	Adz26996 Adeno-sss
45	3453.5	86.6	735	9	ADZ26992	Adz26992 Adeno-sss

ALIGNMENTS

RESULT 1
AAV71167
ID AAV71167 standard; protein; 736 AA.

XX AAV71167;
XX
XX 08-SEP-2000 (first entry)
XX
XX Adeno-associated virus serotype 1 capsid protein VP1.
XX
XX Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
XX cap protein; recombinant viral vector; gene delivery; gene therapy;
XX vaccine; transgene; VP1.
XX
XX Adeno-associated virus 1.
XX
XX
XX PN WO200028061-A2.
XX
XX 18-MAY-2000.
XX
XX 02-NOV-1999; 99WO-US025694.
XX
XX 05-NOV-1998; 98US-0107114P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Wilson JM, Xiao W;
XX
XX WPI, 2000-376571/32.
XX N-PSDB; AAD00772, AAD00777.
XX
XX Novel adeno-associated virus serotype 1 polynucleotide useful for
PT preparation of medicament for delivery of a transgene to a host.
PT
XX
XX Claim 7, Page 87-90; 108pp; English.
XX
XX The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA
XX which is characterised by two inverted terminal repeats (ITR) and open
XX reading frames for rep and capsid (cap) proteins. The rep reading frame
XX encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap
XX reading frame encodes three structural proteins, VP1, VP2 and VP3. The
XX AAV-1 sequence or its fragments particularly ITRs, rep and cap coding
XX regions, are useful in production of recombinant viral vectors for gene
XX delivery. These vectors can be used as gene therapy vectors, vaccine
XX vectors or antisense delivery vectors. The AAV-1 does not induce the
XX formation of neutralising antibodies specific to any serotype of AAV
XX hence is useful for transforming host cells, and in the preparation of a

medicament for the delivery of transgene to a host. The present sequence is an AAV-1 cap protein Vp1 which is useful in the production of recombinant viral vector for gene delivery

Sequence 736 AA;

Query Match 100.0%; Score 3989; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 4,9e-311;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAADGYLPDMLEDNLSGIRREWMDLKPGAPKPKANQOKODDGRGLVLPGYRYLGPFGNLD 60
DB 1 MAADGYLPDMLEDNLSGIRREWMDLKPGAPKPKANQOKODDGRGLVLPGYRYLGPFGNLD 60
OY 61 KGEPNADAAALHEDKAYDQOLKAGDNPYLRYNHADAEPFERLOEDTSPGANTGRAVFO 120
DB 61 KGEPNADAAALHEDKAYDQOLKAGDNPYLRYNHADAEPFERLOEDTSPGANTGRAVFO 120
OY 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTGOOPAKKRLNFGQTGDS 180
DB 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTGOOPAKKRLNFGQTGDS 180
OY 181 SVDPDQPLGEBPPATPAVGPPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVI 240
DB 181 SVDPDQPLGEBPPATPAVGPPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVI 240
OY 241 TTSPTTMAALPTYNHNLKYQISSASTGASNDNHRYGYSTPMKGFDPNRRHCHFSPPDMQRL 300
DB 241 TTSPTTMAALPTYNHNLKYQISSASTGASNDNHRYGYSTPMKGFDPNRRHCHFSPPDMQRL 300
OY 301 INNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQ 360
DB 301 INNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQ 360
OY 361 GCLPPFPADVPMIPOYGYLTLLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTFSYTFEEVP 420
DB 361 GCLPPFPADVPMIPOYGYLTLLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTFSYTFEEVP 420
OY 421 FHSSTYAHQSQSLDRLNPLIDQYLYLNRTONQSGSAQNKDILFSGSPAGMSVOPKMWLP 480
DB 421 FHSSTYAHQSQSLDRLNPLIDQYLYLNRTONQSGSAQNKDILFSGSPAGMSVOPKMWLP 480
OY 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCV 540
DB 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCV 540
OY 541 MIFGKESAGASNTALDNVTIDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG 600
DB 541 MIFGKESAGASNTALDNVTIDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG 600
OY 601 ALPGVWQDRODVYLOGPTIMAKIPHTDGHFHPSPLMGFGGLKNPPQIILIKTTPVANPAPA 660
DB 601 ALPGVWQDRODVYLOGPTIMAKIPHTDGHFHPSPLMGFGGLKNPPQIILIKTTPVANPAPA 660
OY 661 EFSATKFAFSITQYSTQGVSEIEMELOKENSKRNNPEVQYTSNKAASANDFTDNNGL 720
DB 661 EFSATKFAFSITQYSTQGVSEIEMELOKENSKRNNPEVQYTSNKAASANDFTDNNGL 720
OY 721 YTEPPPIGTRVLTPL 736
DB 721 YTEPPPIGTRVLTPL 736

```

RESULT 2
ABB80232
ID ABB80232 standard; protein; 736 AA.

XX ABB80232;
XX AC
XX 20-NOV-2003 (first entry)
XX AAV1 vp1 protein.
XX

KW Adeno-associated virus; AAV; serotype 9; rep; cap; vp1; vp2; vp3;
KW splice variant; transgene.

OS Adeno associated virus serotype 1.

XX WO2003052052-A2.

XX 26-JUN-2003.

XX 12-NOV-2002; 2002WO-US033631.

XX 17-DEC-2001; 2001US-0341150P.

XX 05-JUN-2002; 2002US-0386132P.

XX (TYPE-) UNIV PENNSYLVANIA.

XX Gao G, Wilson JM, Alvira M;

XX WPI; 2003-523523/49.

XX New isolated adeno-associated virus (AAV) comprising an AAV capsid.

XX Useful for preparing a medicament for delivering a transgene to a cell.

XX Disclosure; Fig 2; 76pp; English.

The sequences given in ABB80231-34 represent vp1 proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three protein vp1, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene to a cell

XX Sequence 736 AA;

Query Match 100.0%; Score 3989; DB 6; Length 736;
Best Local Similarity 100.0%; Pred. No. 4,9e-311;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAADGYLPDMLEDNLSGIRREWMDLKPGAPKPKANQOKODDGRGLVLPGYRYLGPFGNLD 60
DB 1 MAADGYLPDMLEDNLSGIRREWMDLKPGAPKPKANQOKODDGRGLVLPGYRYLGPFGNLD 60
OY 61 KGEPNADAAALHEDKAYDQOLKAGDNPYLRYNHADAEPFERLOEDTSPGANTGRAVFO 120
DB 61 KGEPNADAAALHEDKAYDQOLKAGDNPYLRYNHADAEPFERLOEDTSPGANTGRAVFO 120
OY 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTGOOPAKKRLNFGQTGDS 180
DB 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTGOOPAKKRLNFGQTGDS 180
OY 181 SVDPDQPLGEBPPATPAVGPPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVI 240
DB 181 SVDPDQPLGEBPPATPAVGPPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVI 240
OY 241 TTSPTTMAALPTYNHNLKYQISSASTGASNDNHRYGYSTPMKGFDPNRRHCHFSPPDMQRL 300
DB 241 TTSPTTMAALPTYNHNLKYQISSASTGASNDNHRYGYSTPMKGFDPNRRHCHFSPPDMQRL 300
OY 301 INNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQ 360
DB 301 INNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQ 360
OY 361 GCLPPFPADVPMIPOYGYLTLLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTFSYTFEEVP 420
DB 361 GCLPPFPADVPMIPOYGYLTLLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTFSYTFEEVP 420
OY 421 FHSSTYAHQSQSLDRLNPLIDQYLYLNRTONQSGSAQNKDILFSGSPAGMSVOPKMWLP 480
DB 421 FHSSTYAHQSQSLDRLNPLIDQYLYLNRTONQSGSAQNKDILFSGSPAGMSVOPKMWLP 480
OY 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCV 540

```

Db 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMSCV 540
QY 541 MIFGKESAGASNTALDNVMTDEBEIKATNPVATERFGTVAVNFQSSSTDPAIGVHANG 600
Db 541 MIFGKESAGASNTALDNVMTDEBEIKATNPVATERFGTVAVNFQSSSTDPAIGVHANG 600
QY 601 ALPGMWQDRDYLQGPITWAKI PHTDGHFHPSPLMGFGELKNPPQILIKNTVPVNPAP 660
Db 601 ALPGMWQDRDYLQGPITWAKI PHTDGHFHPSPLMGFGELKNPPQILIKNTVPVNPAP 660
QY 661 EFSATKFAFITQYSTGVSVLEIWELOKENSKRNPVEVQYTSNVAKSANVDFTVNNGL 720
Db 661 EFSATKFAFITQYSTGVSVLEIWELOKENSKRNPVEVQYTSNVAKSANVDFTVNNGL 720
QY 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736
RESULT 3
ID ABR62762 standard; protein; 736 AA.
AC ABR62762;
DT 06-NOV-2003 (first entry)
DE Adeno associated virus 1 capsid protein vpl.
KW AAV; AAV1; capsid; vector; gene therapy; antisense therapy; vaccine.
XX
XX
XX Adeno associated virus.
OS
PN MO2003052051-A2.
XX
XX 26-JUN-2003.
PF 12-NOV-2002; 2002MO-US033630.
XX
PR 17-DEC-2001; 2001US-0341151P.
PR 01-MAY-2002; 2002US-0377133P.
PR 05-JUN-2002; 2002US-0386122P.
XX
XX (UYPR-) UNIV PENNSYLVANIA.
XX
PI Gao G, Wilson JM, Alviria M;
XX
XX WPI; 2003-523522/49.
XX
XX New adeno-associated virus (AAV) comprising an AAV capsid having an amino
PT acid sequence of AAV8, useful for preparing a medicament for delivery of
PT a transgene to a cell and for treating cystic fibrosis or hemophilia B.
XX
XX
XX Disclosure; Fig 2A-C; 82pp; English.
XX
XX The present sequence is the protein sequence of the vpl capsid protein of
CC adeno associated virus serotype 1 (AAV1). The invention provides the
CC nucleic acid and amino acid sequences of novel AAV8 and fragments of
CC these sequences. Each of these fragments may be used in a variety of
CC vector systems and host cells. Among the desirable fragments are the cap
CC proteins, including vpl, vp2, vp3 and hypervariable regions, the rep
CC proteins, including rep78, rep68, rep52 and rep40, and the sequences
CC encoding these proteins. The fragments may be used alone, in combination
CC with other AAV8 sequences or in combination with elements from other AAV
CC or non-AAV sequences in the production of recombinant AAV and for
CC use as antisense delivery vectors, gene therapy vectors or vaccine
CC vectors. A claimed molecule comprises a cap protein of a functional AAV
CC rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and
CC AAV6
XX
SQ Sequence 736 AA;
Query Match 100.0%; Score 3989; DB 7; Length 736;

Best Local Similarity 100.0%; Pred. No. 4,9e-311;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAADGVLPMWEDINSEIGIREWMDLKPGAPYRKANQOQODDGRGLVFGYKLGSPFNGLD 60
Db 1 MAADGVLPMWEDINSEIGIREWMDLKPGAPYRKANQOQODDGRGLVFGYKLGSPFNGLD 60
QY 61 KGEVNAADAAALEHDKAYDQOLKAGDNPYLRVNHADAEFOERLOEDTSPGSLGRAVFO 120
Db 61 KGEVNAADAAALEHDKAYDQOLKAGDNPYLRVNHADAEFOERLOEDTSPGSLGRAVFO 120
QY 121 AKKRVLBEPLGLVEEAKTAPGKKRPVEQSPOEPPSSSIGIKTGOQPAKKRLNFGQTGSE 180
Db 121 AKKRVLBEPLGLVEEAKTAPGKKRPVEQSPOEPPSSSIGIKTGOQPAKKRLNFGQTGSE 180
QY 181 SVDPDQPLGEPPTPAVGPPTTMASGGAPMADNNEGADGVGNASGNHCDSTWLGDRYI 240
Db 181 SVDPDQPLGEPPTPAVGPPTTMASGGAPMADNNEGADGVGNASGNHCDSTWLGDRYI 240
QY 241 TTSRTMALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGTFDNRHCHFSPPDMQRL 300
Db 241 TTSRTMALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGTFDNRHCHFSPPDMQRL 300
QY 301 INNNGFPPKRLNFKLFENIQVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLSAQH 360
Db 301 INNNGFPPKRLNFKLFENIQVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLSAQH 360
QY 361 GCLPFPADVPMIPOYGYLLTNNGSOAVGRSSFCLEYFPSSQMLRTGNNFTSYFEEVP 420
Db 361 GCLPFPADVPMIPOYGYLLTNNGSOAVGRSSFCLEYFPSSQMLRTGNNFTSYFEEVP 420
QY 421 FHSSTAHQSOLRLNPNPLIDQYLLYNRTQNSSGAKNDLLFSRGSPPAGMVGOPKNWLP 480
Db 421 FHSSTAHQSOLRLNPNPLIDQYLLYNRTQNSSGAKNDLLFSRGSPPAGMVGOPKNWLP 480
QY 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMSCV 540
Db 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMSCV 540
QY 541 MIFGKESAGASNTALDNVMTDEBEIKATNPVATERFGTVAVNFQSSSTDPAIGVHANG 600
Db 541 MIFGKESAGASNTALDNVMTDEBEIKATNPVATERFGTVAVNFQSSSTDPAIGVHANG 600
QY 601 ALPGMWQDRDYLQGPITWAKI PHTDGHFHPSPLMGFGELKNPPQILIKNTVPVNPAP 660
Db 601 ALPGMWQDRDYLQGPITWAKI PHTDGHFHPSPLMGFGELKNPPQILIKNTVPVNPAP 660
QY 661 EFSATKFAFITQYSTGVSVLEIWELOKENSKRNPVEVQYTSNVAKSANVDFTVNNGL 720
Db 661 EFSATKFAFITQYSTGVSVLEIWELOKENSKRNPVEVQYTSNVAKSANVDFTVNNGL 720
QY 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736
RESULT 4
ID ADE76565 standard; protein; 736 AA.
AC ADE76565;
DT 29-JAN-2004 (first entry)
DE Adeno-associated virus (AAV) related protein, SEQ ID No 64.
XX
XX adeno-associated virus; AAV; cytosaric; antiposaric; antitubercular;
XX antitubercular; neuroprotective; antidiabetic; antichytoid;
XX dermatological; antineoplastic; gene therapy; vaccine;
XX hyperproliferative; cancer; psoriasis; autoimmune disease;
XX rheumatoid arthritis; multiple sclerosis; diabetes;
XX autoimmune thyroiditis; scleroderma; Crohn's disease.
XX

OS Unidentified.
 XX EPI310571-A2.
 PN
 PD 14-MAY-2003.
 XX
 XX 12-NOV-2002; 2002EP-00257826.
 PF
 PR 13-NOV-2001; 2001US-0350607P.
 PR 17-DEC-2001; 2001US-0341117P.
 PR 01-MAY-2002; 2002US-0377066P.
 PR 05-JUN-2002; 2002US-0386675P.
 XX
 PA (UNPE-) UNIV PENNSYLVANIA.
 XX
 PI Gao G, Wilson JM, Alvira M;
 DR WPI; 2003-450984/43.
 XX
 XX
 PT Detecting adeno-associated virus sequences in a sample, useful for e.g.
 PT preventing or treating hyperproliferative or autoimmune diseases,
 PT comprises subjecting a sample having a DNA to amplification via
 PT polymerase chain reaction.
 XX
 PS Disclosure; SEQ ID NO 64; 419pp; English.
 XX
 CC The invention relates to a novel method for detecting adeno-associated
 CC virus (AAV) sequences in a sample, which comprises subjecting a sample
 CC containing a DNA to amplification via a polymerase chain reaction (PCR).
 CC The AAV sequence have the following activities: cytostatic,
 CC antiproliferatic, antitumoric, antidiabetic, neuroprotective,
 CC antidiabetic, antihypertoid, dermatological, and antiinflammatory. The AAV
 CC sequence can be used in gene therapy or as part of a vaccine to treat
 CC disorders. The method is useful in detecting and/or identifying AAV
 CC sequences and isolating novel sequences that are identified. The
 CC sequences may be used e.g. for preventing or treating hyperproliferative
 CC conditions such as cancers and psoriasis, and other autoimmune diseases
 CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
 CC chryoiditis, scleroderma or Crohn's disease. This sequence represents an
 CC AAV related protein sequence of the invention.
 XX
 XX Sequence 736 AA;
 SQ
 Query Match 100.0%; Score 3989; DB 7; Length 736;
 Best Local Similarity 100.0%; Pred. No. 4.9e-311;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAADGYLPDWEEDNTLSEGIREWMDLKPAPKPKANQKQDDRGGLVLPQYKYLGFPGILD 60
 DB 1 MAADGYLPDWEEDNTLSEGIREWMDLKPAPKPKANQKQDDRGGLVLPQYKYLGFPGILD 60
 QY 61 KCEPNAADAALHDKAVDQOLKAGDNPYLRYNADAFQORLQEDPISFGNLGRAVFO 120
 DB 61 KCEPNAADAALHDKAVDQOLKAGDNPYLRYNADAFQORLQEDPISFGNLGRAVFO 120
 QY 121 AKKRVLEPLGLVEBGAKTPAGKRPVEGSPQBPSSSGIGKTGQOPAKKRLNFGQTGSE 180
 DB 121 AKKRVLEPLGLVEBGAKTPAGKRPVEGSPQBPSSSGIGKTGQOPAKKRLNFGQTGSE 180
 QY 122 AKKRVLEPLGLVEBGAKTPAGKRPVEGSPQBPSSSGIGKTGQOPAKKRLNFGQTGSE 180
 DB 122 AKKRVLEPLGLVEBGAKTPAGKRPVEGSPQBPSSSGIGKTGQOPAKKRLNFGQTGSE 180
 QY 181 SVDPDQPLGEBPPATPAVGPPTTMASSGGA PMADNNEGADGVNAGNMHCSTWLGDYVI 240
 DB 181 SVDPDQPLGEBPPATPAVGPPTTMASSGGA PMADNNEGADGVNAGNMHCSTWLGDYVI 240
 QY 241 TTSTRTMALPTYNHLYKQISASTGASNDNHYFGYSTWGFDPNRPFHCHSPDWORL 300
 DB 241 TTSTRTMALPTYNHLYKQISASTGASNDNHYFGYSTWGFDPNRPFHCHSPDWORL 300
 QY 301 INNNGFRPKRLNFKLNFQVKEVYTTNDGVTIANNLSTVQVFPDSEYQLPYVLSAHO 360
 DB 301 INNNGFRPKRLNFKLNFQVKEVYTTNDGVTIANNLSTVQVFPDSEYQLPYVLSAHO 360
 QY 361 GCLPPFPADVFMIPQYGYLTLLNGSOAVGRSSFYCLEYPPSQMLRTGNNTFSYTFEEVP 420

DB 361 GCLPPFPADVFMIPQYGYLTLLNGSOAVGRSSFYCLEYPPSQMLRTGNNTFSYTFEEVP 420
 QY 421 FHSSVYASQSLDRMLNPLIDQVLYYLNRTONOGSQAQNKDLFSRGS PAGMSVQPKNMLP 480
 DB 421 FHSSVYASQSLDRMLNPLIDQVLYYLNRTONOGSQAQNKDLFSRGS PAGMSVQPKNMLP 480
 QY 481 GPCYRQQRVSKYTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCV 540
 DB 481 GPCYRQQRVSKYTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCV 540
 QY 541 MIFGKESAGASNTALDVMITDDEEIKATNPVATERGTAAVNFOSSTDPATGDVAMG 600
 DB 541 MIFGKESAGASNTALDVMITDDEEIKATNPVATERGTAAVNFOSSTDPATGDVAMG 600
 QY 601 ALPGMWQDRDVLQGPIMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTVPANPPA 660
 DB 601 ALPGMWQDRDVLQGPIMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTVPANPPA 660
 QY 661 EFSATKFASTITQYSTQVSEIEMELQKNSKRMNPEVOYTSNYSKAVDFTVNNGL 720
 DB 661 EFSATKFASTITQYSTQVSEIEMELQKNSKRMNPEVOYTSNYSKAVDFTVNNGL 720
 QY 721 YTEPRPIGTRYLTRPL 736
 DB 721 YTEPRPIGTRYLTRPL 736
 RESULT 5
 ADV70294
 ID ADV70294 standard; protein; 736 AA.
 XX
 XX ADV70294;
 DT 10-MAR-2005 (first entry)
 XX
 XX Primate adeno-associated virus 1 capsid protein VP1.
 DE
 XX immunosuppressive; gene therapy; immunogenicity; virus inactivation;
 XX hemophilia; Pepco deficiency; galactosemia; phenylketonuria;
 KW Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
 KW atherosclerosis; thrombosis; embolism; Parkinson's disease;
 KW congestive heart failure; cancer; inflammation; immune disorder;
 KW muscular dystrophy; diabetes; VPI.
 KW
 OS Adeno-associated virus 1.
 XX
 XX WO2004112727-A2.
 PN
 PD 29-DEC-2004.
 XX
 PF 21-JUN-2004; 2004WO-US019884.
 PR 19-JUN-2003; 2003US-0480395P.
 PR 30-APR-2004; 2004US-0567310P.
 PR 03-JUN-2004; 2004US-0576501P.
 XX
 XX (AVIG-) AVIGEN INC.
 PA
 PI Arbetman AE, Colosi P, Lochrie MA, Surosky RT;
 DR WPI; 2005-048755/05.
 XX
 XX
 PT New mutated adeno-associated virus (AAV) capsid protein that when present
 PT in an AAV viron imparts decreased immunoreactivity to the viron as
 PT compared to the corresponding wild-type viron, useful for treating e.g.
 PT hemophilia.
 PT
 XX
 PS Example 5; SEQ ID NO 20; 136pp; English.
 XX
 CC The invention describes a mutated adeno-associated virus (AAV) capsid
 CC protein that when present in an AAV viron imparts decreased
 CC immunoreactivity to the viron as compared to the corresponding wild-type
 CC viron. Also described are: a polynucleotide encoding the mutated protein

Db	6	KGEVNAADAALAEHKAVDQQLKAGDNPYLRYLNHDAEAFQERLQEDPISFCGNLGRAVFG	120
Qy	121	AKKRVLEPLGLVEBGAKTKAPGKKRPVEOSPOEDSSGIGTKGQAPAKRLNFCQTGDS	180
Db	121	AKKRVLEPLGLVEBGAKTKAPGKKRPVEOSPOEDSSGIGTKGQAPAKRLNFCQTGDS	180
Qy	181	SVDDPOPLGEPPTPAVAGPTTMAAGGAPMADNNEGADGAGNASGMNHCSTLGDRI	240
Db	181	SVDDPOPLGEPPTPAVAGPTTMAAGGAPMADNNEGADGAGNASGMNHCSTLGDRI	240
Qy	241	TTSTRWALPTYNNHLKYKISSASTGASNDNHYFGYSTPMGYPDENRPHCFSPRDMQRL	300
Db	241	TTSTRWALPTYNNHLKYKISSASTGASNDNHYFGYSTPMGYPDENRPHCFSPRDMQRL	300
Qy	301	INNMGFRPRRLNFKLPIQVKEVTTNDGVTTLANNLTSTVQVPSDSHYQLPYLGSAGQ	360
Db	301	INNMGFRPRRLNFKLPIQVKEVTTNDGVTTLANNLTSTVQVPSDSHYQLPYLGSAGQ	360
Qy	361	GCLRPFPADVFMIPQGYGLTLNNGSAVGRSFFCLEFPPQMLRTGNPFSTFEV	420
Db	361	GCLRPFPADVFMIPQGYGLTLNNGSAVGRSFFCLEFPPQMLRTGNPFSTFEV	420
Qy	421	FHSYSYASOSLDLMLNPLIDQLYLYNRTQNSGSAQNKDILFSRSPAGMSVQPKMLP	480
Db	421	FHSYSYASOSLDLMLNPLIDQLYLYNRTQNSGSAQNKDILFSRSPAGMSVQPKMLP	480
Qy	481	GPCYRQQRVSKTDTNNNSNFTWTGASKTNLGRESIINPGTAMASHKDEKFFPMG	540
Db	481	GPCYRQQRVSKTDTNNNSNFTWTGASKTNLGRESIINPGTAMASHKDEKFFPMG	540
Qy	541	MIRKESAGASNTALNNWITDEEELKATNPATERFGTVAVNNQSSSTDPAATGDVAMG	600
Db	541	MIRKESAGASNTALNNWITDEEELKATNPATERFGTVAVNNQSSSTDPAATGDVAMG	600
Qy	601	ALPQMWDQDDVYLQGPRIWAKIPHTGTHFHPSPLMGFGGLKNPPOILIKTPIVNPAPPA	660
Db	601	ALPQMWDQDDVYLQGPRIWAKIPHTGTHFHPSPLMGFGGLKNPPOILIKTPIVNPAPPA	660
Qy	661	EFSAITKASPIITQYSTGVQSVIEIEMELQKENSKRNNPEVQYTSNYAKSANDVFTDNNGL	720
Db	661	EFSAITKASPIITQYSTGVQSVIEIEMELQKENSKRNNPEVQYTSNYAKSANDVFTDNNGL	720
Qy	721	YTERPRPIGTRVLTTRPL 736	
Db	721	YTERPRPIGTRVLTTRPL 736	
RESULT 7			
AD227012			
ID	AD227012	standard; protein; 736 AA.	
XX	AC		
XX	AD227012;		
XX	DT		
XX	30-JUN-2005	(first entry)	
DE	Adeno-associated virus protein SEQ ID NO 162.		
XX			
XX	rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;		
KW	scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;		
KW	bacterial infection; cancer; ulcerative colitis; antidiabetic;		
KW	antiarthritic; neuroprotective; antiinflammatory; antidiabetic;		
KW	antiproliferative; vasodilator; gastrointestinal-gen.; hemostatic; anti-HIV;		
KW	virucide; antibacterial; cytostatic; antitumor; dermatological.		
XX			
OS	Adeno-associated virus.		
XX			
PN	MO200503321-A2.		
XX			
PD	14-APR-2005.		
XX			
PF	30-SEP-2004; 2004MO-US028817.		
XX			
PR	30-SEP-2003; 2003US-0508226P.		

XX	29-Apr-2004; 2004US-0566546P.
XX	(UTPE-) UNIV PENNSYLVANIA.
XX	
PI	Wilson JM, Gao G, Alvira MR, Vandenberghc LH;
XX	WPI; 2005-265437/29.
DR	
XX	
PT	New adeno-associated virus (AAV) clade comprising at least three AAV
PT	members, useful for preventing and/or treating arthritis, multiple
PT	sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
PT	infection and cancer.
XX	
PS	Disclosure; SEQ ID NO 162; 569pp: English.
XX	
CC	The invention relates to an adeno-associated virus (AAV) clade comprising
CC	at least three AAV members, where each member of the AAV clade is
CC	phylogenetically related as determined using a Neighbor-Joining heuristic
CC	by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
CC	correction distance measurement of no more than 0.05. The methods and
CC	compositions of the present invention are useful for the prevention
CC	and/or treatment of rheumatoid arthritis, multiple sclerosis,
CC	sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
CC	disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
CC	colitis. The present sequence represents the amino acid sequence of an
XX	adeno-associated virus protein.
XX	
SQ	Sequence 736 AA;
Query Match	100.0%; Score 3989; DB 9; Length 736;
Best Local Similarity	100.0%; Pred. No. 4,9e-311;
Matches 736; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAADGYLPDWLIEDNLSGIREWMDLKFGABKPYANQKODGGGLVPGYYLGPFGNLD 60
DB	1 MAADGYLPDWLEDNLSGIREWMDLKFGABKPYANQKODGGGLVPGYYLGPFGNLD 60
QY	61 KGEVNAADAALAEHDKAYVOQLKAGNPLYLRYNHDAEFOERLOEDTSFGNMGRAVFO 120
DB	61 KGEVNAADAALAEHDKAYVOQLKAGNPLYLRYNHDAEFOERLOEDTSFGNMGRAVFO 120
QY	121 AKKRVLPPLIGIVEGAKTAPGKKRPVQSSQOEPPSSGIGIKTGOQPAKKXLNFGQTDSE 180
DB	121 AKKRVLPPLIGIVEGAKTAPGKKRPVQSSQOEPPSSGIGIKTGOQPAKKXLNFGQTDSE 180
QY	181 SVPDPQELGEBPATPAVVGPTTMASSGGGAPMADNNEGADVGNAAGNMHCDSTWLGDRVI 240
DB	181 SVPDPQELGEBPATPAVVGPTTMASSGGGAPMADNNEGADVGNAAGNMHCDSTWLGDRVI 240
QY	241 TTSTRTMALPTYNHNLKYQIISASTGASNDNHFGYSTPMGYFDENRFFCHFSFPRMQRL 300
DB	241 TTSTRTMALPTYNHNLKYQIISASTGASNDNHFGYSTPMGYFDENRFFCHFSFPRMQRL 300
QY	301 INNMMGRPRRLNKLFNIOQKEVTTMDGYTTANNLSTVVOVFSDEYOLPYVLGSAHQ 360
DB	301 INNMMGRPRRLNKLFNIOQKEVTTMDGYTTANNLSTVVOVFSDEYOLPYVLGSAHQ 360
QY	361 GCLPPPADVPMIOYGYLTLNNGSAQVGRSSFYCLEYFPSSOMLRTGNNTFFSYTFEEVP 420
DB	361 GCLPPPADVPMIOYGYLTLNNGSAQVGRSSFYCLEYFPSSOMLRTGNNTFFSYTFEEVP 420
QY	421 FHSSVYASOSLDRMLNPLIDQYLYLNRTONQSGAANKULLFSGSPAGMSVQPKWLP 480
DB	421 FHSSVYASOSLDRMLNPLIDQYLYLNRTONQSGAANKULLFSGSPAGMSVQPKWLP 480
QY	481 GPCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESLIINGTAMASHKDEDEKFFPMISGV 540
DB	481 GPCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESLIINGTAMASHKDEDEKFFPMISGV 540
QY	541 MIPKESAGASNTLNDVMFTDDEEIKATNPVATERGTAAVNFQSSSTDPATGDVHANG 600
DB	541 MIPKESAGASNTLNDVMFTDDEEIKATNPVATERGTAAVNFQSSSTDPATGDVHANG 600

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QY      601 ALPGMWQDRDYLQGPIMAKIPTHGHRHPSPLMGFGLKNPPOILLKNTVPANPPA 660
      |||||||
DB      601 ALPGMWQDRDYLQGPIMAKIPTHGHRHPSPLMGFGLKNPPOILLKNTVPANPPA 660
QY      661 EFSATKFAFTIQTSTGQVSEIEMELQKENSCKRNKPEVQYTSNVAKSANVPTVDNNGL 720
      |||||||
DB      661 EFSATKFAFTIQTSTGQVSEIEMELQKENSCKRNKPEVQYTSNVAKSANVPTVDNNGL 720
QY      721 YTEPRPIGTRYLTRPL 736
      |||||||
DB      721 YTEPRPIGTRYLTRPL 736
      |||||||

RESULT 8
ADV67506
ADV67506 standard; protein; 735 AA.
AC      ADV67506;
XX
XX      10-MAR-2005 (first entry)
XX
XX      Amino acid sequence of the capsid protein of AAV serotype 1.
XX      antiarteriosclerotic; antilipemic; gene therapy; cholesterol;
XX      apolipoprotein E; apoe; apolipoprotein A; apoa; atherosclerosis;
XX      lipoprotein defect; capsid protein.
XX      Adeno-associated virus.
XX      MO2004108922-A2.
XX      16-DEC-2004.
XX      23-APR-2004; 2004MO-US010965.
XX      25-APR-2003; 2003US-0465293P.
XX      (UYPE-) UNIV PENNSYLVANIA.
XX      Rader DJ, Wilson JM;
XX      WPI; 2005-031700/03.
XX
XX      Lowering total cholesterol levels and treating atherosclerosis in a
XX      subject comprises delivering a recombinant adeno-associated virus (AAV)
XX      comprising an AAV serotype capsid protein or a gene encoding human
XX      apolipoprotein E (apoE) or apoA.
XX
XX      Disclosure; SEQ ID NO 4; 69pp; English.
XX
XX      The specification describes a method for lowering total cholesterol
XX      levels in a subject. The method comprises delivering to the subject a
XX      recombinant adeno-associated virus (AAV) comprising a gene encoding a
XX      human apolipoprotein E (apoE) or apoA under the control of a regulatory
XX      control sequence which directs expression of the gene. The recombinant
XX      AAV also comprises a capsid protein selected from an AAV serotype (e.g.
XX      AAV7 or AAV6) which preferentially expresses high levels of transgene in
XX      liver. A therapeutically effective amount of apoE or apoA expression is
XX      obtained upon delivery of low dose of AAV. The method of the invention is
XX      useful for lowering total cholesterol levels in a subject, e.g. for
XX      treating atherosclerosis, and for correcting defects in lipoprotein. The
XX      present sequence represents a capsid protein of AAV serotype 1 (AAV1),
XX      which may be used in recombinant AAV vectors of the invention.
XX
XX      Sequence 735 AA;
XX
Query Match      99.9%; Score 3985; DB 9; Length 735;
Best Local Similarity 100.0%; Pred. No. 1e-310;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MAADGYLPDWLENDLSGIRRMWDLKGPAPKPKANQKODDGRGLVPGKYVIGPENGDL 60
      |||||||
DB      1 MAADGYLPDWLENDLSGIRRMWDLKGPAPKPKANQKODDGRGLVPGKYVIGPENGDL 60
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QY      61 KGEPVNAADAAALEHDKAYDQDLKAGDNPYLRYNHADAEFOERLQEDTSFGNLAGRAVQ 120
      |||||||
DB      61 KGEPVNAADAAALEHDKAYDQDLKAGDNPYLRYNHADAEFOERLQEDTSFGNLAGRAVQ 120
QY      121 AKKRVLEPLGLVEEAKTAPGKKRPVEQSPOEPPSSGIGKTGOQPAKKRLNFGQTGDE 180
      |||||||
DB      121 AKKRVLEPLGLVEEAKTAPGKKRPVEQSPOEPPSSGIGKTGOQPAKKRLNFGQTGDE 180
QY      181 SVDPDQPIGEPPTATPAVGPPTTMASGGGAPMADNNEGADGNGNAGSNHCDSTWLGDRYI 240
      |||||||
DB      181 SVDPDQPIGEPPTATPAVGPPTTMASGGGAPMADNNEGADGNGNAGSNHCDSTWLGDRYI 240
QY      241 TTSTRTWMLPTYNHNLXYQOISSAGSNDNHYFGYSTPMGWFDENRPFCHSPDMOQL 300
      |||||||
DB      241 TTSTRTWMLPTYNHNLXYQOISSAGSNDNHYFGYSTPMGWFDENRPFCHSPDMOQL 300
QY      301 INNNMGFPRPKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDBSEYQLPYVLSAHQ 360
      |||||||
DB      301 INNNMGFPRPKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDBSEYQLPYVLSAHQ 360
QY      361 GCLPFPADVFEMIPOGYVLTLLNGSQAVGRSSFYCLEIYFPSCMLRTGNNFTSYTPEEVP 420
      |||||||
DB      361 GCLPFPADVFEMIPOGYVLTLLNGSQAVGRSSFYCLEIYFPSCMLRTGNNFTSYTPEEVP 420
QY      421 FHSSTYAHQSGLDRLMNPLIDQVLYLNRTRQNGSGAQNQDILFSGSSPAGMSVOPKNWLP 480
      |||||||
DB      421 FHSSTYAHQSGLDRLMNPLIDQVLYLNRTRQNGSGAQNQDILFSGSSPAGMSVOPKNWLP 480
QY      481 GPCYRQQRYSKTKTNNNSNFTWTGASKYNLGRSSIINPGTAMASHKDEDEKFPMSGV 540
      |||||||
DB      481 GPCYRQQRYSKTKTNNNSNFTWTGASKYNLGRSSIINPGTAMASHKDEDEKFPMSGV 540
QY      541 MIFGKESAGASNTALDNWMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGVHANG 600
      |||||||
DB      541 MIFGKESAGASNTALDNWMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGVHANG 600
QY      601 ALPGMWQDRDYLQGPIMAKIPTHGHRHPSPLMGFGLKNPPOILLKNTVPANPPA 660
      |||||||
DB      601 ALPGMWQDRDYLQGPIMAKIPTHGHRHPSPLMGFGLKNPPOILLKNTVPANPPA 660
QY      661 EFSATKFAFTIQTSTGQVSEIEMELQKENSCKRNKPEVQYTSNVAKSANVPTVDNNGL 720
      |||||||
DB      661 EFSATKFAFTIQTSTGQVSEIEMELQKENSCKRNKPEVQYTSNVAKSANVPTVDNNGL 720
QY      721 YTEPRPIGTRYLTRP 735
      |||||||
DB      721 YTEPRPIGTRYLTRP 735
      |||||||

RESULT 9
AD227007
AD227007 standard; protein; 736 AA.
AC      AD227007;
XX
XX      30-JUN-2005 (first entry)
XX
XX      Adeno-associated virus protein SEQ ID NO 157.
XX
XX      rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
XX      scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
XX      bacterial infection; cancer; ulcerative colitis; antineoplastic;
XX      antiautistic; neuroprotective; antiinflammatory; antidiabetic;
XX      antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
XX      virucide; antibacterial; cytostatic; antulcer; dermatological.
XX
XX      Adeno-associated virus.
XX      MO2005033321-A2.
XX      14-APR-2005.
XX
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PF 30-SEP-2004; 2004MO-US028817.
 XX
 PR 30-SEP-2003; 2003US-0508226P.
 PR 29-APR-2004; 2004US-056546P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Wilson JM, Gao G, Alvira MR, Vandenbergh LH;
 XX WPI, 2005-285437/29.
 DR
 XX New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.
 XX
 PS Claim 19, SEQ ID NO 157; 569pp; English.
 XX
 CC The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX
 SQ Sequence 736 AA;
 Query Match 99.5%; Score 3968; DB 9; Length 736;
 Best Local Similarity 99.3%; Pred. No. 2.4e-309;
 Matches 731; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MAADGTLPDWLENDLSEGIKREWMDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPFGNGLD 60
 DB 1 MAADGTLPDWLENDLSEGIKREWMDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPFGNGLD 60
 QY 61 KGEPVNADAAALHDKAYDQOLKAGDNPLYLRVNHADAFOERLOEDTSPGNGLGRAVFO 120
 DB 61 KGEPVNADAAALHDKAYDQOLKAGDNPLYLRVNHADAFOERLOEDTSPGNGLGRAVFO 120
 QY 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEOSPQSDSSSGIKGQGPAPKRLNFGQTGSE 180
 DB 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEOSPQSDSSSGIKGQGPAPKRLNFGQTGSE 180
 QY 181 SVDPDQPLGEPPTAAVPTTMAAGGAPMADNNEGADGVNAGSNHCHDSTWLGDRVI 240
 DB 181 SVDPDQPLGEPPTAAVPTTMAAGGAPMADNNEGADGVNAGSNHCHDSTWLGDRVI 240
 QY 241 TTSTRTWALPTVNNHLYKOISSASTGASNDNHYFGYSTPFWGYFDNRPCHFSPPDWRL 300
 DB 241 TTSTRTWALPTVNNHLYKOISSASTGASNDNHYFGYSTPFWGYFDNRPCHFSPPDWRL 300
 QY 301 INNMGFRKRLNFKLNFQVEKVTNNOVTIANNLSTVQVPSDSEYQLPYVLSAHQ 360
 DB 301 INNMGFRKRLNFKLNFQVEKVTNNOVTIANNLSTVQVPSDSEYQLPYVLSAHQ 360
 QY 361 GCLPPFPADVPMIPOYGYTLTNNGSOAVGRSSFYCLEYPSQMLRTGNFTSYFEEVP 420
 DB 361 GCLPPFPADVPMIPOYGYTLTNNGSOAVGRSSFYCLEYPSQMLRTGNFTSYFEEVP 420
 QY 421 FHSSVAHSGSLDRLNMLIDQYLYLNRTQNGSGAQNKDLLPSRGSPPAGMSVQPNWLP 480
 DB 421 FHSSVAHSGSLDRLNMLIDQYLYLNRTQNGSGAQNKDLLPSRGSPPAGMSVQPNWLP 480
 QY 481 GGCYQQRASKTKTDNNNSNFTWTGASKYNLNGRBSIIRPTGMAASHDDEKFFPMGCV 540
 DB 481 GGCYQQRASKTKTDNNNSNFTWTGASKYNLNGRBSIIRPTGMAASHDDEKFFPMGCV 540
 QY 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFTVAVNFQSSSTDPATGDVHAMG 600

DB 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFTVAVNFQSSSTDPATGDVHAMG 600
 QY 601 ALPGMWODDDVYQGIWAKIPHTDGHFHPSPIMGFGGLKNPPOLIKNTPPANPPA 660
 DB 601 ALPGMWODDDVYQGIWAKIPHTDGHFHPSPIMGFGGLKNPPOLIKNTPPANPPA 660
 QY 661 EFSATKRFASFTQSTQGVSEIEMELQKNSKRMNPEVOYTSNVAKSANVDFTVNNGL 720
 DB 661 EFSATKRFASFTQSTQGVSEIEMELQKNSKRMNPEVOYTSNVAKSANVDFTVNNGL 720
 QY 721 YTEBRPIGTRYLRPL 736
 DB 721 YTEBRPIGTRYLRPL 736
 RESULT 10
 AAB59847
 ID AAB59847 standard; protein; 736 AA.
 XX
 AC AAB59847;
 DT 28-MAR-2001 (first entry)
 XX
 DE AAV6 capsid protein VP1.
 XX
 KW AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;
 KW atherosclerosis; sickle cell anaemia; chalassemia;
 KW blood clotting disorder; diabetes; capsid protein VP1.
 XX
 OS Adeno associated virus.
 XX
 PN US6156303-A.
 PD 05-DEC-2000.
 XX
 PF 11-JUN-1997; 97US-00873168.
 XX
 PR 11-JUN-1997; 97US-00873168.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Russell DW, Rutledge EA;
 XX
 DR WPI, 2001-060164/07.
 XX
 PT Adeno-associated virus serotype 6 and viral vector derived from it for
 PT gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
 PT syndrome, sickle cell anemia, chalassemia and diabetes.
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present invention relates to adeno-associated virus serotypes. The
 CC present sequence is capsid protein VP1 of one such serotype (AAV6). AAV6
 CC can be used to construct AAV viral vectors for use in gene therapy for a
 CC range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,
 CC sickle cell anaemia, thalassemia, blood clotting disorders and diabetes.
 CC The AAV viral vectors have increased transduction efficiency of a
 CC particular host cell as the AAV virion containing the AAV vector genome
 CC can be modified to express a capsid protein of an AAV serotype that
 CC transduces the selected host cell
 XX
 SQ Sequence 736 AA;
 Query Match 99.3%; Score 3963; DB 4; Length 736;
 Best Local Similarity 99.2%; Pred. No. 6.1e-309;
 Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MAADGTLPDWLENDLSEGIKREWMDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPFGNGLD 60
 DB 1 MAADGTLPDWLENDLSEGIKREWMDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPFGNGLD 60
 QY 61 KGEPVNADAAALHDKAYDQOLKAGDNPLYLRVNHADAFOERLOEDTSPGNGLGRAVFO 120

[illegible]

	Query Match	99.3%;	Score 3963;	DB 7;	Length 736;	
	Best Local Similarity	99.2%;	Pred. No. 6.1e-309;			
	Matches 730;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0	
QY	1	MAADGYLPELWLEDNLSGIREWMDIKPGAPKPKANQOKODDGRGLVLPQYKYLGPNGID	60			
DB	1	MAADGYLPELWLEDNLSGIREWMDIKPGAPKPKANQOKODDGRGLVLPQYKYLGPNGID	60			
QY	61	KGEPPNADAALAEHDKAYDOOLKAGDNPYLRYNHADADEFORLEDDTSFGGNLGAAYPO	120			
DB	61	KGEPPNADAALAEHDKAYDOOLKAGDNPYLRYNHADADEFORLEDDTSFGGNLGAAYPO	120			
QY	121	AKKRLAEPLGLVEBGAKTAPGKKRVEBOSPOEDSSSGIGKYGQOPAKKRLNFGQGDSE	180			
DB	121	AKKRLAEPLGLVEBGAKTAPGKKRVEBOSPOEDSSSGIGKYGQOPAKKRLNFGQGDSE	180			
QY	181	SVPDPQLGEBEPATEAAYGPTTMASSGGGAPMADNNEGADGVNAGSGNWHCDSTWLGDRYI	240			
DB	181	SVPDPQLGEBEPATEAAYGPTTMASSGGGAPMADNNEGADGVNAGSGNWHCDSTWLGDRYI	240			
QY	241	TTSTRTMALPTYNNHLKYQISSASGASINDNHYFGYSTPTWGYEDFRRFHCHSPRMOML	300			
DB	241	TTSTRTMALPTYNNHLKYQISSASGASINDNHYFGYSTPTWGYEDFRRFHCHSPRMOML	300			
QY	301	INNNGGPPPKRLNFKLFENIQVEKVTINDGVTTIANNLSTVQVFPDSEYQLPYVLGSAHQ	360			
DB	301	INNNGGPPPKRLNFKLFENIQVEKVTINDGVTTIANNLSTVQVFPDSEYQLPYVLGSAHQ	360			
QY	361	GCLPFPADVEMIPQYGYLTLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTESYTFEBVP	420			
DB	361	GCLPFPADVEMIPQYGYLTLNNGSOAVGRSSFYCLEYFPQMLRTGNNFTESYTFEBVP	420			
QY	421	FHSSTAHOSQSLRLNPNPLIDQYLYTLNRRQONSQGANQNDLLFSRSGPAGMSVQPKWLP	480			
DB	421	FHSSTAHOSQSLRLNPNPLIDQYLYTLNRRQONSQGANQNDLLFSRSGPAGMSVQPKWLP	480			
QY	481	GCYCAQOQRASKTKTDNNNSNFTWTGASKNVLNGRESIIPGTAMASHKDDKDFPMSGV	540			
DB	481	GCYCAQOQRASKTKTDNNNSNFTWTGASKNVLNGRESIIPGTAMASHKDDKDFPMSGV	540			

DB 481 GPCYRQGVSKTKTDNNNSFTWTGASKYKLNGBESSINPGTAMASHKDDKFFPMGCV 540
QY MIFGKESGASNTALDNNMTDEBEIKATNPATPERFCTVAVNPSSSTDPATGDVHMG 600
DB 541 MIFGKESGASNTALDNNMTDEBEIKATNPATPERFCTVAVNPSSSTDPATGDVHMG 600
QY 601 ALPGWVQDRDVLVLOGPIWAKIPHTDGFHPSPLMGFGGLKNPFPQILIKNTVPANPPA 660
DB 601 ALPGWVQDRDVLVLOGPIWAKIPHTDGFHPSPLMGFGGLKNPFPQILIKNTVPANPPA 660
QY 661 EFSATKFSFTTQVSTGVSVIEIWELOKENSCKMNPVOTTSNYSKASANDFTYDNNGL 720
DB 661 EFSATKFSFTTQVSTGVSVIEIWELOKENSCKMNPVOTTSNYSKASANDFTYDNNGL 720
QY 721 YTEPRPIGTRVLRPL 736
DB 721 YTEPRPIGTRVLRPL 736
RESULT 12
ADV70293
ID ADV70293 standard: protein: 736 AA.
XX
AC ADV70293;
XX
DT 10-MAR-2005 (first entry)
XX
DE Primate adeno-associated virus 6 capsid protein VPI.
XX
KW immunosuppressive; gene therapy; immunogenicity; virus inactivation;
KW hemophilia; Pepck deficiency; galactosemia; phenylketonuria;
KW Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
KW atherosclerosis; thrombosis; embolism; Parkinson's disease;
KW congestive heart failure; cancer; inflammation; immune disorder;
KW muscular dystrophy; diabetes; VPI.
XX
OS Adeno-associated virus 6.
XX
PN MO200412727-A2.
XX
PD 29-DEC-2004.
XX
PF 21-JUN-2004; 2004MO-US019884.
XX
PR 19-JUN-2003; 2003US-0480395P.
PR 30-APR-2004; 2004US-0567310P.
PR 03-JUN-2004; 2004US-0576501P.
XX
PA (AVIG-) AVIGEN INC.
XX
PI Arbetman AE, Colosi P, Lochrie MA, Surosky RT;
XX
DR WPI, 2005-048755/05.
XX
PT New mutated adeno-associated virus (AAV) capsid protein that when present
PT in an AAV virion imparts decreased immunoreactivity to the virion as
PT compared to the corresponding wild-type virion, useful for treating e.g.
PT hemophilia.
XX
PS Example 5; SEQ ID NO 19; 136pp; English.
XX
CC The invention describes a mutated adeno-associated virus (AAV) capsid
CC protein that when present in an AAV virion imparts decreased
CC immunoreactivity to the virion as compared to the corresponding wild-type
CC virion. Also described are: a polynucleotide encoding the mutated protein
CC above; a recombinant AAV virion comprising the mutated protein above; and
CC delivering a recombinant AAV virion to a cell or tissue of a vertebrate
CC subject. The recombinant AAV virion is useful for delivering a
CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate
CC subject, where the protein encoded by the heterologous nucleic acid
CC molecule is expressed at a level that provides a therapeutic effect.
CC where the recombinant AAV virion may comprise a non-primate, mammalian
CC AAV capsid protein that when present in an AAV virion imparts decreased

CC immunoreactivity to the virion as compared to immunoreactivity of primate
CC AAV-2, and the heterologous nucleic acid molecule, where the heterologous
CC nucleic acid molecule encodes a therapeutic protein and is operably
CC linked to control elements capable of directing the in vivo transcription
CC and translation of the protein. The protein or the recombinant AAV virion
CC is useful for treating or preventing a wide variety of disorders such as
CC hemophilia, glycogen storage deficiency type 1A, pepck deficiency,
CC galactosemia, phenylketonuria, Crigler-Najjar disease, Gout and Leach-
CC Nyen syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis,
CC thrombosis, embolisms, Parkinson's disease, congestive heart failure,
CC cancer, inflammatory and immune disorders, muscular dystrophies, and
CC diabetes. This is the amino acid sequence of adeno-associated virus 6
CC (AAV6) capsid protein VPI.
XX
SQ Sequence 736 AA;

Query Match 99.34; Score 3963; DB 9; Length 736;
Best Local Similarity 99.24; Pred. No. 6,1e-309;
Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAADGYLPMWLENDLSEGIREFMMDLKPGAPKPKANOOKODDGRGLVPGYKYLGPFGGLD 60
DB 1 MAADGYLPMWLENDLSEGIREFMMDLKPGAPKPKANOOKODDGRGLVPGYKYLGPFGGLD 60
QY 61 KGEFVNADAALAEHDKAYDQOLKAGDNPYLRYNHADAEPQERLQEDTSPFGNIGRAVFQ 120
DB 61 KGEFVNADAALAEHDKAYDQOLKAGDNPYLRYNHADAEPQERLQEDTSPFGNIGRAVFQ 120
QY 121 AKKRVLEPLGLVERGAKTAPGKKRPVROSPOEPPSSGIGRTGQOQPAKKRLNFCQTGSE 180
DB 121 AKKRVLEPLGLVERGAKTAPGKKRPVROSPOEPPSSGIGRTGQOQPAKKRLNFCQTGSE 180
QY 181 SVPPQPLGEPFAPPAVGPPTMASGGGAPADNNEGADVGNSGNWCHDSTWLGDRVI 240
DB 181 SVPPQPLGEPFAPPAVGPPTMASGGGAPADNNEGADVGNSGNWCHDSTWLGDRVI 240
QY 241 TTSRTMALPTYNHLLYKQISSASTGASNDNHVGYSTPMWGFDFNRFCHFSPRDWQL 300
DB 241 TTSRTMALPTYNHLLYKQISSASTGASNDNHVGYSTPMWGFDFNRFCHFSPRDWQL 300
QY 301 INNNWGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVPSDSSEYQLPYVLGSAHQ 360
DB 301 INNNWGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVPSDSSEYQLPYVLGSAHQ 360
QY 361 GCLPPFADVFMIOYGYLTLNNGSOAVGRSFFCLETFPSQMLRTGNPFTFTFEEDVP 420
DB 361 GCLPPFADVFMIOYGYLTLNNGSOAVGRSFFCLETFPSQMLRTGNPFTFTFEEDVP 420
QY 421 FHSSVAHSQSLDRMLNPLIDQYLYLNKTQNGSQAOKKDLFSRGSFAGMSVOPKMLP 480
DB 421 FHSSVAHSQSLDRMLNPLIDQYLYLNKTQNGSQAOKKDLFSRGSFAGMSVOPKMLP 480
QY 481 GPCYRQGVSKTKTDNNNSFTWTGASKYKLNGBESSINPGTAMASHKDDKFFPMGCV 540
DB 481 GPCYRQGVSKTKTDNNNSFTWTGASKYKLNGBESSINPGTAMASHKDDKFFPMGCV 540
QY 541 MIFGKESGASNTALDNNMTDEBEIKATNPATPERFCTVAVNPSSSTDPATGDVHMG 600
DB 541 MIFGKESGASNTALDNNMTDEBEIKATNPATPERFCTVAVNPSSSTDPATGDVHMG 600
QY 601 ALPGWVQDRDVLVLOGPIWAKIPHTDGFHPSPLMGFGGLKNPFPQILIKNTVPANPPA 660
DB 601 ALPGWVQDRDVLVLOGPIWAKIPHTDGFHPSPLMGFGGLKNPFPQILIKNTVPANPPA 660
QY 661 EFSATKFSFTTQVSTGVSVIEIWELOKENSCKMNPVOTTSNYSKASANDFTYDNNGL 720
DB 661 EFSATKFSFTTQVSTGVSVIEIWELOKENSCKMNPVOTTSNYSKASANDFTYDNNGL 720
QY 721 YTEPRPIGTRVLRPL 736
DB 721 YTEPRPIGTRVLRPL 736

RESULT 13

AD227070 standard; protein; 736 AA.

AD227070;

30-JUN-2005 (first entry)

Adeno-associated virus protein SEQ ID NO 220.

XX rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 XX scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 KW bacterial infection; cancer; ulcerative colitis; antineoplastic;
 KW antitubercular; neuroprotective; antiinflammatory; antidiabetic;
 KW antipneumococcal; vasotropic; gastrointestinal; gen.; hemostatic; anti-HIV;
 KW virucide; antibacterial; cytostatic; antitumor; dermatological.

Adeno-associated virus.

MO2005033321-A2.

14-APR-2005.

30-SEP-2004; 2004MO-US028817.

30-SEP-2003; 2003US-0508226P.

29-APR-2004; 2004US-0566546P.

(UNP-) UNIV PENNSYLVANIA.

Wilson JM, Gao G, Alvira MR, Vandenberghe LH;

WPI; 2005-285437/29.

XX New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.

Disclosure; SEQ ID NO 220; 569pp; English.

XX The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.

Sequence 736 AA:

Query Match 99.3%; Score 3963; DB 9; Length 736;

Best Local Similarity 99.2%; Pred. No. 6.1e-309;

Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

1 MAADGYLPDWLENDLSEGREWMDLKPAPKPRANQOKDDGRLVLPKYKYLGPFGD 60

1 MAADGYLPDWLENDLSEGREWMDLKPAPKPRANQOKDDGRLVLPKYKYLGPFGD 60

61 KGEFVNAADAAALEHDKAYNOOLKAGNPLYRNHDAEFOERLQEDTSFGNLSGRAVQ 120

61 KGEFVNAADAAALEHDKAYNOOLKAGNPLYRNHDAEFOERLQEDTSFGNLSGRAVQ 120

121 AKKRVLEPLGLIVEGATAPGKRRPVQSSQIEPSSSGIGTGGQPAKKRLNFGQTGDS 180

121 AKKRVLEPLGLIVEGATAPGKRRPVQSSQIEPSSSGIGTGGQPAKKRLNFGQTGDS 180

181 SVDPQPLGEPAPPAVGPPTMASGGAPMADNNEGADGVGNAGNHCDSITWLGDRVI 240

DB 181 SVDPQPLGEPAPPAVGPPTMASGGAPMADNNEGADGVGNAGNHCDSITWLGDRVI 240

QY 241 TTSITRTMALPTYYNNHLYQIISASGASNDNHYPGISTPMWGFEDNRRFHCHSPRDMQRL 300

DB 241 TTSITRTMALPTYYNNHLYQIISASGASNDNHYPGISTPMWGFEDNRRFHCHSPRDMQRL 300

QY 301 INNMWGFPRKRLNFEFLFNIQVKEVTTNDGVTIANNLSTVQVPSDSEYQLPYVLSGAHQ 360

DB 301 INNMWGFPRKRLNFEFLFNIQVKEVTTNDGVTIANNLSTVQVPSDSEYQLPYVLSGAHQ 360

QY 361 GCLPFPADVFMIPQYGLTLNNGSQAVGRSFFCYLBFPSQMLRTGNNFTFSYFEEBP 420

DB 361 GCLPFPADVFMIPQYGLTLNNGSQAVGRSFFCYLBFPSQMLRTGNNFTFSYFEEBP 420

QY 421 FHSSTYAHQSGLDRLNPLIDQYLYLANTQONOSGAKNDLLFSRGSFAGMSVQKMLP 480

DB 421 FHSSTYAHQSGLDRLNPLIDQYLYLANTQONOSGAKNDLLFSRGSFAGMSVQKMLP 480

QY 481 GPCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDKPFPMGCV 540

DB 481 GPCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDKPFPMGCV 540

QY 541 MIFGESAGASNTALDNWMTDEEIKATNPVATERFGTVAVNFQSSSTDPAITGVHANG 600

DB 541 MIFGESAGASNTALDNWMTDEEIKATNPVATERFGTVAVNFQSSSTDPAITGVHANG 600

QY 601 ALPGWVQDRDYLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILIKNTPVPANPPA 660

DB 601 ALPGWVQDRDYLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILIKNTPVPANPPA 660

QY 661 EFSATKFPASFTIYQSTGVSVIEIWELOKENSKRNNPEVQYTSNYSKANSANVPTVNNGL 720

DB 661 EFSATKFPASFTIYQSTGVSVIEIWELOKENSKRNNPEVQYTSNYSKANSANVPTVNNGL 720

QY 721 YTEPRPIGRTYLRPL 736

DB 721 YTEPRPIGRTYLRPL 736

RESULT 14

AD227086 standard; protein; 737 AA.

AD227086;

30-JUN-2005 (first entry)

Adeno-associated virus protein SEQ ID NO 236.

XX rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 KW scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 KW bacterial infection; cancer; ulcerative colitis; antineoplastic;
 KW antitubercular; neuroprotective; antiinflammatory; antidiabetic;
 KW antipneumococcal; vasotropic; gastrointestinal; gen.; hemostatic; anti-HIV;
 KW virucide; antibacterial; cytostatic; antitumor; dermatological.

Adeno-associated virus.

MO2005033321-A2.

30-SEP-2004; 2004MO-US028817.

30-SEP-2003; 2003US-0508226P.

29-APR-2004; 2004US-0566546P.

(UNP-) UNIV PENNSYLVANIA.

Wilson JM, Gao G, Alvira MR, Vandenberghe LH;

WPI; 2005-285437/29.

PT New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.

XX Claim 19; SEQ ID NO 236; 569pp; English.

CC The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.

CC Sequence 737 AA;

Query Match 97.7%; Score 3897.5; DB 9; Length 737;

Best Local Similarity 97.7%; Pred. No. 1.1e-303; Indels 1; Gaps 1;
 Matches 720; Conservative 6; Mismatches 10;

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QY 1 MAADGYLPMWLEDNISEGIREWMDLKPGAPRKANQKODDGRGLVLPGYKYLGPFGNLD 60
DB 1 MAADGYLPMWLEDNISEGIREWMDLKPGAPRKANQKODDGRGLVLPGYKYLGPFGNLD 60
QY 61 KGEPVNAADAALBHDKAYDQOLKAGDNPYLRYNHADAEPORLOEDTSPFGNIGRAVFO 120
DB 61 KGEPVNAADAALBHDKAYDQOLKAGDNPYLRYNHADAEPORLOEDTSPFGNIGRAVFO 120
QY 121 AKKRVLEPLGLVEBGAKTAPGKRKRVESPO-EPDSSSGIGCTGQOPAKKRLNFGQTDS 179
DB 121 AKKRVLEPLGLVEBGAKTAPGKRKRVESPO-EPDSSSGIGCTGQOPAKKRLNFGQTDS 180
QY 180 ESVPPDPPGEBPPATPAVPTTMAAGGAPMADNNEGADGVGNAGMWHCDSTLGRV 239
DB 181 ESVPPDPPGEBPPATPAVPTTMAAGGAPMADNNEGADGVGNAGMWHCDSTLGRV 240
QY 240 ITTSTRYALPTYNHLYKQISSASTGASNDNHYFGYSTPMGYPFDPNRFCHFSPRDWR 299
DB 241 ITTSTRYALPTYNHLYKQISSASTGASNDNHYFGYSTPMGYPFDPNRFCHFSPRDWR 300
QY 300 LINNMGRPRKLNKRLPIQYKRYTNDGVTIANNLSTYQVSDSEYOLPYVLGSAH 359
DB 301 LINNMGRPRKLNKRLPIQYKRYTNDGVTIANNLSTYQVSDSEYOLPYVLGSAH 360
QY 360 QGCLPPPADVPMIYQYGLTLNNGSOAVGRSSFYCLREYFPMQMLRTGNFTFSYTFEBV 419
DB 361 QGCLPPPADVPMIYQYGLTLNNGSOAVGRSSFYCLREYFPMQMLRTGNFTFSYTFEBV 420
QY 420 PFHSSVYAHQSJLDRMLNPLIDQYLYLNRTQNGSSAQNKDLLFSGSPAGMSVOPKMWL 479
DB 421 PFHSSVYAHQSJLDRMLNPLIDQYLYLNRTQNGSSAQNKDLLFSGSPAGMSVOPKMWL 480
QY 480 BGPCTVROORVSTKTDNNNSNFTWVGASKYNLNGRESIINPCTAASHDDDKFFPMSG 539
DB 481 BGPCTVROORVSTKTDNNNSNFTWVGASKYNLNGRESIINPCTAASHDDDKFFPMSG 540
QY 540 VMIPEGESAGSNTALDNVMTDEBEIKATNPVATERFGTVAVNFOSSSTDATGDVAM 599
DB 541 VMIPEGESAGSNTALDNVMTDEBEIKATNPVATERFGTVAVNFOSSSTDATGDVAM 600
QY 600 GALPGMWMODRDVYLGPIWAKIPHTDGHFSPPLMGFGGLKNPPQILIKTTPVANPP 659
DB 601 GALPGMWMODRDVYLGPIWAKIPHTDGHFSPPLMGFGGLKNPPQILIKTTPVANPP 660
QY 660 AAFSATKFASTITQYSTGVSVIEIWELOKENSKEWNPVOTTSYASANDFTVDNNG 719
DB 661 AAFSATKFASTITQYSTGVSVIEIWELOKENSKEWNPVOTTSYASANDFTVDNNG 720

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QY 720 LYTEPRPIGTRYLTRPL 736
 DB 721 LYTEPRPIGTRYLTRPL 737

RESULT 15

ID AD227010 standard; protein; 737 AA.

AC AD227010;

DT 30-JUN-2005 (first entry)

DE Adeno-associated virus protein SEQ ID NO 160.

KM rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 KM scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 KM bacterial infection; cancer; ulcerative colitis; anti-rheumatic;
 KM antiarthritic; neuroprotective; anti-inflammatory; antidiabetic;
 KM antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
 KM virucide; antibacterial; cytostatic; antiulcer; dermatological.

OS Adeno-associated virus.

PN WO200503321-A2.

PD 14-APR-2005.

PF 30-SEP-2004; 2004WO-US028817.

PR 30-SEP-2003; 2003US-0508226P.

PR 29-APR-2004; 2004US-0566546P.

PA (UNPE-) UNIV PENNSYLVANIA.

PI Wilson JM, Gao G, Alvira MR, Vandenberghe LH;

DR WPI; 2005-285437/29.

PT New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.

PS Claim 46; SEQ ID NO 160; 569pp; English.

CC The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.

CC Sequence 737 AA;

Query Match 97.4%; Score 3883.5; DB 9; Length 737;

Best Local Similarity 97.4%; Pred. No. 1.5e-302; Indels 1; Gaps 1;
 Matches 718; Conservative 6; Mismatches 12;

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QY 1 MAADGYLPMWLEDNISEGIREWMDLKPGAPRKANQKODDGRGLVLPGYKYLGPFGNLD 60
DB 1 MAADGYLPMWLEDNISEGIREWMDLKPGAPRKANQKODDGRGLVLPGYKYLGPFGNLD 60
QY 61 KGEPVNAADAALBHDKAYDQOLKAGDNPYLRYNHADAEPORLOEDTSPFGNIGRAVFO 120
DB 61 KGEPVNAADAALBHDKAYDQOLKAGDNPYLRYNHADAEPORLOEDTSPFGNIGRAVFO 120
QY 121 AKKRVLEPLGLVEBGAKTAPGKRKRVESPO-EPDSSSGIGCTGQOPAKKRLNFGQTDS 179

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Db      121 AKKRVLEPLGLVEAKTAPGKKRPVEPSPORSPPDSSTGIGKKGOQPAKKRLNFGQTGDS 180
QY      180 ESVDPDQPIGEBPPATPAVGPPTMASGGA PMADNNEGADGVNAGSGNWHCDSTWLGDRV 239
Db      181 ESVDPDQPIGEBPPAGSGISGSTMAGGAPMADNNEGADGVNAGSGNWHCDSTWLGDRV 240
QY      240 ITTSTRTMALPTYNNHLYKQISSASTGASNDNHFGYSTPMWGFDPNRFCHFSPRDMOR 299
Db      241 ITTSTRTMALPTYNNHLYKQISSASTGASNDNHFGYSTPMWGFDPNRFCHFSPRDMOR 300
QY      300 LNNMGFRPKLNFLFNIQVKEVTNNGVTTIANNLSTVOVFSDEYOLPYVLGSAH 359
Db      301 LNNMGFRPKLNFLFNIQVKEVTNNGVTTIANNLSTVOVFSDEYOLPYVLGSAH 360
QY      360 OGCLPPFPADVPMIPOYGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYFEEV 419
Db      361 OGCLPPFPADVPMIPOYGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYFEEV 420
QY      420 PFHSSYAHSQSLDRMLNPLIDQYLYYLNRTONQSGSAQNKDLLFSRGSFAGMSVQPKMWL 479
Db      421 PLHSSYAHSQSLDRMLNPLIVQYLYYLNRTONQSGSAQNKDLLFSRGSFAGMSVQPKMWL 480
QY      480 PGFCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMG 539
Db      481 PGFCYRQORVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMG 540
QY      540 VMI FGKESAGASNTALDNVMI TDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM 599
Db      541 VMI FGKESAGASNTALDNVMI TDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM 600
QY      600 GALPGWVWODRDVYLOGPIWAKI PHTDGHFSPPLMGFGGLKNP PPQILIKNTVPANPP 659
Db      601 GALPGWVWODRDVYLOGPIWAKI PHTDGHFSPPLMGFGGLKNP PPQILIKNTVPANPP 660
QY      660 AEFSAITKFASTIQTSTGVSVBIEMWLOKENSRRNPEVQYTSNAXSANDVFTVDNNG 719
Db      661 AEFSAITKFASTIQTSTGVSVBIEMWLOKENSRRNPEVQYTSNAXSANDVFTVDNNG 720
QY      720 LYTEPRPIGTRYLTRPL 736
Db      721 LYTEPRPIGTRYLTRPL 737

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OM protein - protein search, using SW model

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(without alignments)
1817.892 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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- 2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3989	100.0	736	2	US-09-807-802A-3
2	3989	100.0	736	2	US-09-807-802A-13
3	3402.5	85.3	735	2	US-09-321-589-1
4	3402.5	85.3	735	2	US-10-293-478-1
5	3402.5	85.3	735	2	US-10-038-972A-13
6	3251	81.5	735	2	US-09-807-802A-15
7	2906	72.9	534	2	US-09-807-802A-17
8	2759.5	69.2	538	2	US-10-038-972A-14
9	2486.5	62.2	734	2	US-09-532-594B-4
10	2481.5	62.2	533	2	US-10-038-972A-15
11	2220	55.7	724	2	US-09-533-427-4
12	1830.5	45.9	588	2	US-09-532-594B-16
13	1700.5	42.6	588	2	US-09-533-427-5
14	1690.5	42.4	544	2	US-09-532-594B-18
15	1665	41.7	532	2	US-09-533-427-6
16	1410	35.3	756	2	US-09-438-268-4
17	599.5	15.0	781	2	US-10-187-253B-27
18	590.5	14.8	781	2	US-10-187-253B-33
19	486	12.2	554	2	US-10-187-253B-29
20	479.5	12.0	543	2	US-10-187-253B-35
21	430.5	10.8	500	2	US-08-856-841-16
22	430.5	10.8	501	2	US-08-856-841-19
23	429.5	10.8	486	2	US-08-856-841-20
24	326	8.2	415	2	US-08-856-841-13
25	318	8.0	415	2	US-08-856-841-13
26	310	7.8	264	2	US-08-856-841-14
27	310	7.8	264	2	US-08-856-841-14

28	303	7.6	398	2	US-08-856-841-21	Sequence 21, Appl
29	284	7.1	387	2	US-08-856-841-17	Sequence 17, Appl
30	216.5	5.4	579	6	5223424-13	Patent No. 5223424
31	192	4.8	584	2	US-09-022-949-2	Sequence 2, Appl1
32	142	3.6	210	2	US-08-856-841-9	Sequence 9, Appl1
33	142	3.6	227	2	US-08-856-841-15	Sequence 15, Appl
34	142	3.6	250	2	US-08-856-841-12	Sequence 12, Appl
35	132.5	3.3	489	2	US-10-376-397B-4	Sequence 4, Appl1
36	124	3.1	3060	1	US-08-487-826B-14	Sequence 14, Appl
37	122.5	3.1	1637	2	US-10-172-502-14	Sequence 14, Appl
38	121	3.0	2736	2	US-09-252-991A-30227	Sequence 30227, A
39	119.5	3.0	1394	2	US-08-296-791-2	Sequence 2, Appl1
40	119.5	3.0	1394	2	US-09-839-996-2	Sequence 2, Appl1
41	119.5	3.0	1394	2	US-10-080-505-2	Sequence 2, Appl1
42	119.5	3.0	1394	2	US-10-645-655-2	Sequence 2, Appl1
43	119.5	3.0	1394	4	PCT-US95-10661A-2	Sequence 2, Appl1
44	119	3.0	1095	2	US-09-107-532A-3855	Sequence 3855, Ap
45	117.5	2.9	1395	2	US-10-080-505-7	Sequence 7, Appl1

ALIGNMENTS

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RESULT 1
US-09-807-802A-3
; Sequence 3, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Xiao, Weidong
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNVN.03105A
; CURRENT APPLICATION NUMBER: US/09/807,802A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-3
Query Match          100.0%; Score 3989; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAADGYLPDMLDNLSEGRREWMWDLKPGAPKPKANQKODDGRGLVPGYKYLGPNGLD 60
1 MAADGYLPDMLDNLSEGRREWMWDLKPGAPKPKANQKODDGRGLVPGYKYLGPNGLD 60
Db 1 MAADGYLPDMLDNLSEGRREWMWDLKPGAPKPKANQKODDGRGLVPGYKYLGPNGLD 60
QY 61 KGPVNAADAALIEHDKAYDQKAGDNPLYLRNHAADAEFOELQDTSFGNLSGAVFQ 120
61 KGPVNAADAALIEHDKAYDQKAGDNPLYLRNHAADAEFOELQDTSFGNLSGAVFQ 120
Db 61 KGPVNAADAALIEHDKAYDQKAGDNPLYLRNHAADAEFOELQDTSFGNLSGAVFQ 120
QY 121 AKRRVLEPIGLVEGAKTAPGKKRPVEQSPQEDSSSGIGKTGQOPAKKRLNFGOTGDS 180
121 AKRRVLEPIGLVEGAKTAPGKKRPVEQSPQEDSSSGIGKTGQOPAKKRLNFGOTGDS 180
Db 121 AKRRVLEPIGLVEGAKTAPGKKRPVEQSPQEDSSSGIGKTGQOPAKKRLNFGOTGDS 180
QY 181 SVDPQPLGEPATPAVAGPTTMAASGCGAPMADNNEGADGVGASGNMHCSTWLADRV 240
181 SVDPQPLGEPATPAVAGPTTMAASGCGAPMADNNEGADGVGASGNMHCSTWLADRV 240
Db 181 SVDPQPLGEPATPAVAGPTTMAASGCGAPMADNNEGADGVGASGNMHCSTWLADRV 240
QY 241 TTSTRFALPTYNHLYKQISSASTASNDNHFGYSTPWGTFDNRFFCHSPRDMQRL 300
241 TTSTRFALPTYNHLYKQISSASTASNDNHFGYSTPWGTFDNRFFCHSPRDMQRL 300
Db 241 TTSTRFALPTYNHLYKQISSASTASNDNHFGYSTPWGTFDNRFFCHSPRDMQRL 300
QY 301 INNNKPRPRKRLNFKLPTNOKVEVTNDDGVTIANNLSTVVOVFSSEYQLPVLASAHQ 360
301 INNNKPRPRKRLNFKLPTNOKVEVTNDDGVTIANNLSTVVOVFSSEYQLPVLASAHQ 360
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Db 301 INNMGRPRKRLNFKLNIQVKEVTTNDGVTTIANLSTVQVFSDEYQLPYVLGSAHQ 360
Qy 361 GCLPPFADVFMIPOYGYLTLLNGSOAVGRSSFCLEYPFSOMLRTGNFFSTFEV 420
Db 361 GCLPPFADVFMIPOYGYLTLLNGSOAVGRSSFCLEYPFSOMLRTGNFFSTFEV 420
Qy 421 FHSSAHSQSJDLRLMNPILIDQVLYLNRTONOSGAONKDLFSGSPAGMSVOPKMLP 480
Db 421 FHSSAHSQSJDLRLMNPILIDQVLYLNRTONOSGAONKDLFSGSPAGMSVOPKMLP 480
Qy 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMG 540
Db 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMG 540
Qy 541 MIFGKESAGASNTALDNNMTIDESEIKATNPVATERGTYAVNPOSSSTDPATGDVHAMG 600
Db 541 MIFGKESAGASNTALDNNMTIDESEIKATNPVATERGTYAVNPOSSSTDPATGDVHAMG 600
Qy 601 ALPGWVODRDVYLQGPIMAKIPHTDGHFHPSPLMGFGKLNPPQILIKNTPVANPAP 660
Db 601 ALPGWVODRDVYLQGPIMAKIPHTDGHFHPSPLMGFGKLNPPQILIKNTPVANPAP 660
Qy 661 EFSATKRFASFTIYQSTGVSVIEIEMELQKNSKRNPEVOYTSNYAKSANDFTVDNNG 720
Db 661 EFSATKRFASFTIYQSTGVSVIEIEMELQKNSKRNPEVOYTSNYAKSANDFTVDNNG 720
Qy 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736

RESULT 2

US-09-807-802A-13
; Sequence 13, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPVN.03105A
; CURRENT APPLICATION NUMBER: US/09/807,802A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/407,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-13

Query Match 100.0%; Score 3989; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAADGYLPDWLENDLSEGIKRWMDLKPGA PKPKANQOKDDGRGVLPGYKYLGPFGND 60
Db 1 MAADGYLPDWLENDLSEGIKRWMDLKPGA PKPKANQOKDDGRGVLPGYKYLGPFGND 60
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Db 61 KEEPNNAADAAALBHDKAYDQOLKAGDNPYLRYNHADADEFORLQEDTSFGGNLGRAV 120
Qy 121 AKKRVLEPLGLVEGAKTAPGKRPVBSPOBPSSSGIGTKGQOPAKKRLNFGQTGSE 180
Db 121 AKKRVLEPLGLVEGAKTAPGKRPVBSPOBPSSSGIGTKGQOPAKKRLNFGQTGSE 180
Qy 181 SVDPDPLGEPATPAVGPITMASGGGAPMADNNEGADGVNAGNMHCDSTWLGDYV 240
Db 181 SVDPDPLGEPATPAVGPITMASGGGAPMADNNEGADGVNAGNMHCDSTWLGDYV 240

Db 181 SVDPDPLGEPATPAVGPITMASGGGAPMADNNEGADGVNAGNMHCDSTWLGDYV 240
Qy 241 TTSRTALPLYYNNHLLKQISSASTGASNDNHVGYSTPMGYPDPNRFCHFSRDMORL 300
Db 241 TTSRTALPLYYNNHLLKQISSASTGASNDNHVGYSTPMGYPDPNRFCHFSRDMORL 300
Qy 301 INNMGRPRKRLNFKLNIQVKEVTTNDGVTTIANLSTVQVFSDEYQLPYVLGSAHQ 360
Db 301 INNMGRPRKRLNFKLNIQVKEVTTNDGVTTIANLSTVQVFSDEYQLPYVLGSAHQ 360
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Db 361 GCLPPFADVFMIPOYGYLTLLNGSOAVGRSSFCLEYPFSOMLRTGNFFSTFEV 420
Qy 421 FHSSAHSQSJDLRLMNPILIDQVLYLNRTONOSGAONKDLFSGSPAGMSVOPKMLP 480
Db 421 FHSSAHSQSJDLRLMNPILIDQVLYLNRTONOSGAONKDLFSGSPAGMSVOPKMLP 480
Qy 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMG 540
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Db 541 MIFGKESAGASNTALDNNMTIDESEIKATNPVATERGTYAVNPOSSSTDPATGDVHAMG 600
Qy 601 ALPGWVODRDVYLQGPIMAKIPHTDGHFHPSPLMGFGKLNPPQILIKNTPVANPAP 660
Db 601 ALPGWVODRDVYLQGPIMAKIPHTDGHFHPSPLMGFGKLNPPQILIKNTPVANPAP 660
Qy 661 EFSATKRFASFTIYQSTGVSVIEIEMELQKNSKRNPEVOYTSNYAKSANDFTVDNNG 720
Db 661 EFSATKRFASFTIYQSTGVSVIEIEMELQKNSKRNPEVOYTSNYAKSANDFTVDNNG 720
Qy 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736

RESULT 3

US-09-321-589-1
; Sequence 1, Application US/09321589
; Patent No. 6498244
; GENERAL INFORMATION:
; APPLICANT: McARTHUR, JAMES G.
; APPLICANT: PATEL, SALIL D.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/09/321,589
; CURRENT FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Adeno-associated virus
US-09-321-589-1

Query Match 85.3%; Score 3402.5; DB 2; Length 735;
Best Local Similarity 83.3%; Pred. No. 7.2e-290;
Matches 613; Conservative 51; Mismatches 71; Indels 1; Gaps 1;

Qy 1 MAADGYLPDWLENDLSEGIKRWMDLKPGA PKPKANQOKDDGRGVLPGYKYLGPFGND 60
Db 1 MAADGYLPDWLENDLSEGIKRWMDLKPGA PKPKAERHKDSRGVLPGYKYLGPFGND 60
Qy 61 KEEPNNAADAAALBHDKAYDQOLKAGDNPYLRYNHADADEFORLQEDTSFGGNLGRAV 120
Db 61 KEEPNNAADAAALBHDKAYDQOLKAGDNPYLRYNHADADEFORLQEDTSFGGNLGRAV 120
Qy 121 AKKRVLEPLGLVEGAKTAPGKRPVBSPOBPSSSGIGTKGQOPAKKRLNFGQTGSE 180
Db 121 AKKRVLEPLGLVEGAKTAPGKRPVBSPOBPSSSGIGTKGQOPAKKRLNFGQTGAD 180


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DB 181 SVDPDQPLGEPATPAVGPPTTMASGGGAPMADNNEGADVGNASGNHCDSTWLGDRVI 240
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DB 241 TTSTRTMALPTYNHNLHYKQISSOS - GASNDNHFGYSTPMGYFDENRPHCHSPRDMORL 299
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DB 300 INNMGFPRKRLNFKLFNIQVKEVTNDGTTIANNLSTVOVFPDSEYQLPYVLGSAHQ 359
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DB 360 GCLPPPADVPMIPOGYLTLNNGSQAAGRSSFYCLEYFPSSQMLRTGNNFTSYTFEEVP 419
QY 421 FHSSYAHQSGLDRMLNPLIDQYLYLNRTONQSGAONKDLFSGSPAGMSVQPKMWLP 480
DB 420 FHSSYAHQSGLDRMLNPLIDQYLYLNRTONQSGAONKDLFSGSPAGMSVQPKMWLP 479
QY 481 GPCYRQORVSKTNDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMSCV 540
DB 480 GPCYRQORVSKTSADNNSEYSWTGATKTHLNGRDSLVPNGPAMASHKDDDEKFFPMSCV 539
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DB 540 LIFGKGSEKTNVDIEKWMITDEBEIRTNVPATEQYGSVSTNLQGNKQAATADVNTQG 599
QY 601 ALPGMWODRDVYLLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILLKNTFVPANPPA 660
DB 600 VLPGMWODRDVYLLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILLKNTFVPANPPA 659
QY 661 EFSATKFASTFOYSTGOVSVEIEMELQKENSKRMPPEVQYTSNAXKSNVDFVTYNNGL 720
DB 660 TFSAAKFASFTFOYSTGOVSVEIEMELQKENSKRMPPEIQTYSNAXKSNVDFVTYNNGL 719
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QY 721 YTEPRPIGTRYLTRPL 736
DB 720 YSEPRPIGTRYLTRNL 735

RESULT 4
US-10-293-478-1
; Sequence 1, Application US/10293478
; Patent No. 6733757
; GENERAL INFORMATION:
; APPLICANT: PATEL, SALIL D.
; APPLICANT: MCARTHUR, JAMES G.
; TITLE OF INVENTION: ADEMO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/10/293,478
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/321,589
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 735
; TYPE: PR1
; ORGANISM: Adeno-associated virus
US-10-293-478-1
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Query Match 85.3%; Score 3402.5; DB 2; Length 735;
Best Local Similarity 83.3%; Pred. No. 7.2e-290;
Matches 613; Conservative 51; Mismatches 71; Indels 1; Gaps 1;

QY 1 MAADGYLPDWLENDLSEGIREWMDLKPAGPKPKANQOKDDGRGLVLPQYKYLGPFGGLD 60
DB 1 MAADGYLPDWLENDLSEGIREWMDLKPAGPKPKANQOKDDGRGLVLPQYKYLGPFGGLD 60
QY 61 KGEFVNADAAALEHDKAYVQOOLKAGNPPYLYKYNHADAEOERLQERTSGCNLGRAVFO 120
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DB 61 KGEFVNADAAALEHDKAYVQOOLKAGNPPYLYKYNHADAEOERLQERTSGCNLGRAVFO 120
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DB 121 AKKRLLEPLGLVIEBAKTAAPKKRPVBEOSPOEBSSSGIGTGQOPAKKRLNFGOTGSE 180
QY 181 SVDPDQPLGEPATPAVGPPTTMASGGGAPMADNNEGADVGNASGNHCDSTWLGDRVI 240
DB 181 SVDPDQPLGEPATPAVGPPTTMASGGGAPMADNNEGADVGNASGNHCDSTWLGDRVI 240
QY 241 TTSTRTMALPTYNHNLHYKQISSASTGASNDNHFGYSTPMGYFDENRPHCHSPRDMORL 300
DB 241 TTSTRTMALPTYNHNLHYKQISSOS - GASNDNHFGYSTPMGYFDENRPHCHSPRDMORL 299
QY 301 INNMGFPRKRLNFKLFNIQVKEVTNDGTTIANNLSTVOVFPDSEYQLPYVLGSAHQ 360
DB 300 INNMGFPRKRLNFKLFNIQVKEVTNDGTTIANNLSTVOVFPDSEYQLPYVLGSAHQ 359
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DB 360 GCLPPPADVPMIPOGYLTLNNGSQAAGRSSFYCLEYFPSSQMLRTGNNFTSYTFEEVP 419
QY 421 FHSSYAHQSGLDRMLNPLIDQYLYLNRTONQSGAONKDLFSGSPAGMSVQPKMWLP 480
DB 420 FHSSYAHQSGLDRMLNPLIDQYLYLNRTONQSGAONKDLFSGSPAGMSVQPKMWLP 479
QY 481 GPCYRQORVSKTNDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMSCV 540
DB 480 GPCYRQORVSKTSADNNSEYSWTGATKTHLNGRDSLVPNGPAMASHKDDDEKFFPMSCV 539
QY 541 MIFGESAGASNTALDNWMTDEBEIKATNPVATERFGTVAVNFQSSSTDPTGVDYHANG 600
DB 540 LIFGKGSEKTNVDIEKWMITDEBEIRTNVPATEQYGSVSTNLQGNKQAATADVNTQG 599
QY 601 ALPGMWODRDVYLLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILLKNTFVPANPPA 660
DB 600 VLPGMWODRDVYLLQGPIMAKIPHTDGHFHPSPLMGFGCLKNPPOILLKNTFVPANPPA 659
QY 661 EFSATKFASTFOYSTGOVSVEIEMELQKENSKRMPPEVQYTSNAXKSNVDFVTYNNGL 720
DB 660 TFSAAKFASFTFOYSTGOVSVEIEMELQKENSKRMPPEIQTYSNAXKSNVDFVTYNNGL 719
QY 721 YTEPRPIGTRYLTRPL 736
DB 720 YSEPRPIGTRYLTRNL 735
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RESULT 5
US-10-038-972A-13
; Sequence 13, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 735
; TYPE: PR1
; ORGANISM: adeno-associated virus 2 VPI capsid protien
US-10-038-972A-13
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Query Match 85.3%; Score 3402.5; DB 2; Length 735;
Best Local Similarity 83.3%; Pred. No. 7.2e-290;
Matches 613; Conservative 51; Mismatches 71; Indels 1; Gaps 1;

QY 1 MAADGYLPDWLENDLSEGIREWMDLKPAGPKPKANQOKDDGRGLVLPQYKYLGPFGGLD 60
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Db      1 MAADGYLPMWEDLTSEGIROQWMLKPGPPPKPAERHKDSDRGVLPGYKYLGPENGLD 60
Qy      61 KGEPNNAADAALHEDKAYDQDLKAGDNPYLRYNNADAPOERLOEDPSFGANIGRAYFO 120
        61 KGEPNNAADAALHEDKAYDROLDGDNPLKYNADAEPOERLEEDPSFGANIGRAYFO 120
Db      121 AKKRVLBEPLGLVEEGAKTAPGKKRPVBSPOEPDSSSGIGKTGOQPAKKRLNFGQTDSE 180
Qy      121 AKKRVLBEPLGLVEEGAKTAPGKKRPVBSPOEPDSSSGIGKTGOQPAKKRLNFGQTDSE 180
        121 AKKRVLBEPLGLVEEVKTAPGKKRPVBSPOEPDSSSGIGKTGOQPAKKRLNFGQTDAD 180
Db      181 SVDPDQPLGGEPPATPAVGPPTMASGGGAPMADNNEGADGVNASGWNHCDSTLGRVIT 240
Qy      181 SVDPDQPLGGEPPATPAVGPPTMASGGGAPMADNNEGADGVNASGWNHCDSTLGRVIT 240
        181 SVDPDQPLGGEPPATPAVGPPTMASGGGAPMADNNEGADGVNASGWNHCDSTLGRVIT 240
Db      241 TTSTRTMALPTYNHLYKOISSAGSANDNHYFGYSTPMWGFDPNRFCHFSRDMQRL 300
Qy      241 TTSTRTMALPTYNHLYKOISSAGSANDNHYFGYSTPMWGFDPNRFCHFSRDMQRL 300
        241 TTSTRTMALPTYNHLYKOISSAGSANDNHYFGYSTPMWGFDPNRFCHFSRDMQRL 299
Db      301 INNNMGFPKRLNFKLFNIOVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLGSAHQ 360
Qy      301 INNNMGFPKRLNFKLFNIOVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLGSAHQ 360
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Db      361 GCLPPPADVEMIPQYGYTLNNGSQAVGRSSFCLETFPSQMLRTGNNFTFSYTFEEDVP 420
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Db      421 FHSSTAHSGSLDRLNNPLIDQYLYLNTQONSGSAQNKDILFSRGSAPGMSVOPKMWLP 480
Qy      421 FHSSTAHSGSLDRLNNPLIDQYLYLNTQONSGSAQNKDILFSRGSAPGMSVOPKMWLP 480
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Db      481 GPCYRQORVSKTKTNNNSNFTMGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGV 540
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        480 GPCYRQORVSKTSADNNNSFYSGMTGATKYNLNGRDLVNPBPAMASHKDEDEKFPMSGV 539
Db      541 MIFGKESAGASTALDNNMTDEBEIKATNPVATERFGTVAVNFQSSSTDPATGTVHAMG 600
Qy      541 MIFGKESAGASTALDNNMTDEBEIKATNPVATERFGTVAVNFQSSSTDPATGTVHAMG 600
        540 LIFGQKSEKIVNDEIKWMTDEBEIRTNPVATEOYGSVSTNLGRKQAAATAVNFQ 599
Db      601 ALPGWWMORRDVYLQSPIMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTPVANPST 660
Qy      601 ALPGWWMORRDVYLQSPIMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTPVANPST 660
        600 VLPGWWMORRDVYLQSPIMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTPVANPST 659
Db      661 EFSATKFAFSITQYSTGVSVIEWELQKNSKRNPEVQYTSNVAKSANVDFVNNGL 720
Qy      661 EFSATKFAFSITQYSTGVSVIEWELQKNSKRNPEVQYTSNVAKSANVDFVNNGL 720
        660 TFSAKFAFSITQYSTGVSVIEWELQKNSKRNPEIQTYSNNKSNVDFVNTDNGV 719
Db      721 YTEPRPIGTRYLTRPL 736
Qy      721 YTEPRPIGTRYLTRPL 736
        720 YSEPRPIGTRYLTRNL 735
Db      720 YSEPRPIGTRYLTRNL 735

RESULT 6
US-09-807-802A-15
; Sequence 15, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNPVN.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: AAV-1
```

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US-09-807-802A-15
Query Match      81.5%; Score 3251; DB 2; Length 599;
Best Local Similarity 100.0%; Pred. No. 1, 1e-276;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      138 TAPGKKRPVBSPOEPDSSSGIGKTGOQPAKKRLNFGQTDSESVDPQPLGEPATPAA 197
Db      1 TAPGKKRPVBSPOEPDSSSGIGKTGOQPAKKRLNFGQTDSESVDPQPLGEPATPAA 60
Qy      198 VGPPTMASGGGAPMADNNEGADGVNASGWNHCDSTLGRVITTTSTRTMALPTYNHLY 257
Db      61 VGPPTMASGGGAPMADNNEGADGVNASGWNHCDSTLGRVITTTSTRTMALPTYNHLY 120
Qy      258 KOISSASTGASNDNHYFGYSTPMWGFDPNRFCHFSRDMQRLINNNMGFPKRLNFKLF 317
Db      121 KOISSASTGASNDNHYFGYSTPMWGFDPNRFCHFSRDMQRLINNNMGFPKRLNFKLF 180
Qy      318 NIQVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLGSAHQCLPPPADVEMIPQY 377
Db      181 NIQVKEVTTNDGVTTIANNLSTVQVPSDSEYQLPYVLGSAHQCLPPPADVEMIPQY 240
Qy      378 YLTTNNGSQAVGRSSFCLETFPSQMLRTGNNFTFSYTFEEDVPFHSSTAHSGSLDRLNNP 437
Db      241 YLTTNNGSQAVGRSSFCLETFPSQMLRTGNNFTFSYTFEEDVPFHSSTAHSGSLDRLNNP 300
Qy      438 LIIDQYLYLNTQONSGSAQNKDILFSRGSAPGMSVOPKMWLPQPCYRQORVSKTKTDNN 497
Db      301 LIIDQYLYLNTQONSGSAQNKDILFSRGSAPGMSVOPKMWLPQPCYRQORVSKTKTDNN 360
Qy      498 NSNFTMGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FPKESAGASTALDN 557
Db      361 NSNFTMGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FPKESAGASTALDN 420
Qy      558 VMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGTVHAMGLPGWWMORRDVYLQGP 617
Db      421 VMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGTVHAMGLPGWWMORRDVYLQGP 480
Qy      618 IMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTPVANPAPFAFSATKFAFSITQYSTG 677
Db      481 IMAKIPHTDGHFSPPLMGFGGLKNPPQILIKNTPVANPAPFAFSATKFAFSITQYSTG 540
Qy      678 QVSVIEWELQKNSKRNPEVQYTSNVAKSANVDFVNNGLYTEPRPIGTRYLTRPL 736
Db      541 QVSVIEWELQKNSKRNPEVQYTSNVAKSANVDFVNNGLYTEPRPIGTRYLTRPL 599

RESULT 7
US-09-807-802A-17
; Sequence 17, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNPVN.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 534
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-17

Query Match      72.9%; Score 2906; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1, 8e-246;
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Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 203 MASGGGAPMADNNEGADGVGNASGNMHCSTWLGRLVITTSRTTALPTYNHLYKQISS 262
DB 1 MASGGGAPMADNNEGADGVGNASGNMHCSTWLGRLVITTSRTTALPTYNHLYKQISS 60
QY 263 ASTGASNDNHVFGYSTPWGYPDPNRPCHFSPPRDQRLINNMGFPKRLNFKLNIQYK 322
DB 61 ASTGASNDNHVFGYSTPWGYPDPNRPCHFSPPRDQRLINNMGFPKRLNFKLNIQYK 120
QY 323 EYTTNDGVTIANNLITSTVOVSDSEYQLPYVLGSAHQGLPPFPADVMIPOYGLTLN 382
DB 121 EYTTNDGVTIANNLITSTVOVSDSEYQLPYVLGSAHQGLPPFPADVMIPOYGLTLN 180
QY 383 NGSQAVGRSSFYCLEYFPSCMLRTGNNFTFSYTFEEVPHSSVYAHQSGLDRMLNPLIDQY 442
DB 181 NGSQAVGRSSFYCLEYFPSCMLRTGNNFTFSYTFEEVPHSSVYAHQSGLDRMLNPLIDQY 240
QY 443 LYVLNRTQNSGSAQNKDLLFSRGS PAGMSVQPKNMLPGPCYRQORVSKTKTDNNNSFT 502
DB 241 LYVLNRTQNSGSAQNKDLLFSRGS PAGMSVQPKNMLPGPCYRQORVSKTKTDNNNSFT 300
QY 503 WTGASKYNLNGRESITINPGTAMASHKDDDEKFPMSGVMIFGKESAGASNTALDNVMTD 562
DB 301 WTGASKYNLNGRESITINPGTAMASHKDDDEKFPMSGVMIFGKESAGASNTALDNVMTD 360
QY 563 EEEIKATNPVATERFGTAVAVNFOSSSTDPAIGDVHAMGALPGMWODRDVYLQGPIMAKI 622
DB 361 EEEIKATNPVATERFGTAVAVNFOSSSTDPAIGDVHAMGALPGMWODRDVYLQGPIMAKI 420
QY 623 PHTDGHFHPSPILMGFGGLKNPPOILLIKNTVPANPAPAESATKFASTIYOSTGQSVB 682
DB 421 PHTDGHFHPSPILMGFGGLKNPPOILLIKNTVPANPAPAESATKFASTIYOSTGQSVB 480
QY 683 IEMELOKENSKRNPPEVOYTNSNAXASANDFTVDNNGLYTERPRIGTRYLTRPL 736
DB 481 IEMELOKENSKRNPPEVOYTNSNAXASANDFTVDNNGLYTERPRIGTRYLTRPL 534

RESULT 8
US-10-038-972A-14
; Sequence 14, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 598
; TYPE: PR1
; ORGANISM: adeno-associated virus 2 VP2 capsid protien
US-10-038-972A-14

Query Match 69.2%; Score 2759.5; DB 2; Length 598;
Best Local Similarity 82.8%; Pred. No. 1,7e-233;
Matches 495; Conservative 43; Mismatches 59; Indels 1; Gaps 1;
```

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DB 122 QISSGS -GASNDNHVFGYSTPWGYPDPNRPCHFSPPRDQRLINNMGFPKRLNFKLNI 180
QY 319 IQKEVTTNDGVTIANNLITSTVOVSDSEYQLPYVLGSAHQGLPPFPADVMIPOYGY 378
DB 181 IQKEVTTNDGVTIANNLITSTVOVSDSEYQLPYVLGSAHQGLPPFPADVMIPOYGY 240
QY 379 LTLNNGSQA VGRSSFYCLEYFPSCMLRTGNNFTFSYTFEEVPHSSVYAHQSGLDRMLNPL 438
DB 241 LTLNNGSQA VGRSSFYCLEYFPSCMLRTGNNFTFSYTFEEVPHSSVYAHQSGLDRMLNPL 300
QY 439 IDQVLYLNRITQNSGSAQNKDLLFSRGS PAGMSVQPKNMLPGPCYRQORVSKTKTDNNN 498
DB 301 IDQVLYLNRITQNSGSAQNKDLLFSRGS PAGMSVQPKNMLPGPCYRQORVSKTKTDNNN 360
QY 499 SNFTWTGASKYNLNGRESITINPGTAMASHKDDDEKFPMSGVMIFGKESAGASNTALDNV 558
DB 361 SEYSWTGATKYHLNGRDSTLVNPGPAMASHKDDDEKFPMSGVLIFGKQSEKTNVDIEKY 420
QY 559 MTTDEEIKATNPVATERFGTAVAVNFOSSSTDPAIGDVHAMGALPGMWODRDVYLQGP 618
DB 421 MTTDEEIKATNPVATERFGTAVAVNFOSSSTDPAIGDVHAMGALPGMWODRDVYLQGP 480
QY 619 WAKIHTDGHFHPSPILMGFGGLKNPPOILLIKNTVPANPAPAESATKFASTIYOSTGQ 678
DB 481 WAKIHTDGHFHPSPILMGFGGLKNPPOILLIKNTVPANPAPAESATKFASTIYOSTGQ 540
QY 679 VSEVIEEMELOKENSKRNPPEVOYTNSNAXASANDFTVDNNGLYTERPRIGTRYLTRPL 736
DB 541 VSEVIEEMELOKENSKRNPPEVOYTNSNAXASANDFTVDNNGLYTERPRIGTRYLTRPL 598

RESULT 9
US-09-532-594B-4
; Sequence 4, Application US/09532594B
; Patent No. 6468524
; GENERAL INFORMATION:
; APPLICANT: Chordini, John A.
; APPLICANT: Kolin, Robert M.
; APPLICANT: Safer, Brian
; APPLICANT: Davidson, Beverly
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; FILE REFERENCE: 14014.0252U2
; CURRENT APPLICATION NUMBER: US/09/532,594B
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 734
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e =
; NAME/KEY: misc feature
; OTHER INFORMATION: AAV4 capsid protein VP1
US-09-532-594B-4

Query Match 62.3%; Score 2486.5; DB 2; Length 734;
Best Local Similarity 63.5%; Pred. No. 2.3e-209;
Matches 475; Conservative 81; Mismatches 161; Indels 31; Gaps 10;
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0Y 183 FDPDOLGEPATPRAAVGPRTTASGGGAPMADNNBGADVGNGASGNMHCSTYMLGDRVITTT 242
Db 183 PEGSTSG-----AMSDBSEMPAAAGGAAVEGGQGDVGNGASGDMHCSTYSBGHVTTT 236
0Y 243 STRTAAPLPTNNHLLKJOISASATGASNDNHHFGYSTPMQYFPDNRFHCHFSPPDMQRLIN 302
Db 237 STRTAVLPTNNHLLKRLGE-----SIQSTYNGOFSTPMQYFPDNRHCHFSPPDMQRLIN 292
0Y 303 NNMGFRPKRLNKLFINIQVEYVTTNDGVTTIANNLTSTVQVPSDBSEYOLLPYVLGSAHQG 362
Db 293 NNMGFRPKRMVKYKFINIQVEYVTTSGEFTVANNLTSTVQIFADSSYELPYVMDAQEGS 352
0Y 363 LPFPFADVMITQYGV---LTLNNGQAVGRSSFYCLEYFPQOMLRTQNNFTSYFEERY 419
Db 353 LPFPFENDVMVPOYQYCGVLVTNGTSOQOTDRNAFYCLEYFPQOMLRTQNNFTSYFEERY 412
0Y 420 PPHSSVYASQSLDRMLNPLIDQYLYLVNRTQN-----QGSQAQKDLLFSRGSFAGSAVOP 475
Db 413 PPHSMYVYASQSLDRMLNPLIDQYLMLOSTTTGTTIAGATATN---FTKLRRTNSNRK 469
0Y 476 KMWLPGPCYRQORVSKTKTDNNNSNFTWTGAS---KY-----NUNGRESIINPGTAMASHK 528
Db 470 KMWLPGPSSIKQGFSTXTA--NQYKYKIPATGSDBLIKEYETHSTLUDGRWSALTQPPMATAG 527
0Y 528 DDEDKFPFMSGVMITPKESAGASNTALDNVMTIDSEBIAATNVALERTPQTVAVNQSSS 588
Db 528 PADSK--FSNSOCLIPAGKONGNATVPGLTIFTSBBLATATATDIDMCMNLPGQDOSNS 586
0Y 589 TUPATGVDYAMGALPGMVMQODRDVUYOQPIWAKIPTHDGHHSPPLMGGFGLKNPPQIL 648
Db 587 NLPYDRLTALGAVPBMVQNRDITYOGSPIMAKIPTHDGHHSPPLMGGFGLKHPPQIL 646
0Y 649 IONTVPANPAPAFSAFKPASFITQYSTQGVSEIEMELOKENSXKNMPEVQYTTSNYAKS 708
Db 647 IONTVPANPAPATFSSSTPVNSFITQYSTQGVSOQIMELOKERSXKNMPEVQYTTSNYQO 706
0Y 709 ANVDFTVDNNGLYTERPIGTRYLTPPL 736
Db 707 NSILMAPDAAGXYTERPRAIGTRYLTHHL 734

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US-10-038-972A-15
/ Sequence 15, Application US/10038972A
/ Patent No. 6962815
/ GENERAL INFORMATION:
/ APPLICANT: J. Bartlett
/ TITLE OF INVENTION: AAV VECTORS AND METHODS
/ FILE REFERENCE: 28335/36996US
/ CURRENT APPLICATION NUMBER: US/10/038,972A
/ CURRENT FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: US 60/260,124
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 533
/ TYPE: PR1
/ ORGANISM: adenov-associated virus 2 VP3 capsid protein
US-10-038-972A-15

Query Match      62.2%; Score 2481.5; DB 2; Length 533;
Best Local Similarity 83.3%; Pred. No. 3,7e-209;
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1

Qy      203 MASGGGAPADNNNEGADGVGNASGNWCHGSTYLADGEVITTSRTTALPTYYNNHLYQOISS 262
      1 MATGSGAPADNNNEGADGVGNSSGNWCHGSTWMDGRVITTSRTTALPTYYNNHLYQOISS 60
Db
263 ASTGASNDNHRYGYSTPMWGYPDFNRPHCHFSPPDWORLLINNWWGFRPKLNFYLFNIQVK 322
Qy
61 QS-QASNDNHRYGYSTPMWGYPDFNRPHCHFSPPDWORLLINNWWGFRPKLNFYLFNIQVK 119

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QY	323	EYTTNDGVTITANNLTSTVQVSSDEBYOLPYLGSAGHOCLEPPPADVMIPQYGLTLN	382
Db	120	EYTONDGVTITANNLTSTVQVFTDBEYOLPYLGSAGHOCLEPPPADVMIPQYGLTLN	179
QY	383	NGSQAVGRSSFYCLEYFSPQMRTNNFTFSYTFEEVPHSSAHSQSLDRLLNPLIDQY	442
Db	180	NGSQAVGRSSFYCLEYFSPQMRTNNFTFSYTFEEVPHSSAHSQSLDRLLNPLIDQY	239
QY	443	LYYLNRTONQSGSAONKDLLFSRGSBPAGMSVOPKWLPGPCTRQQRVSKTKTDNNNSFT	502
Db	240	LYYLSRTNTPSGTITTTQSRLOFQOAGASDIRDQSRNMLPGPCYRQOQVSKTSADNNNSYS	299
QY	503	WTGSKYNLNGEESIINPGTAMASHKXDEDKFPPMSGVMI PGKESAGSNTLADNYITD	562
Db	300	WTGATKYHLNGDSLVPNGPAMASHKXDEKEFPQSGVLI PGQOQSEKTNVDLEKMYITD	359
QY	563	EBEITATPVATERFGTVAVNFQSSSTDPATQDVAHMGALPGKVMQDRDVTYLOGPIWAKI	622
Db	360	EBEITATPVATERQVGSVSTNLQKRNROAAITADVNTQVLPKVMQDRDVTYLOGPIWAKI	419
QY	623	PHTHGHFSPIMGFGFGLKNPPQILIKNTPVANPAPAEFSATKEAFTTQYSTQGVSVF	682
Db	420	PHTHGHFSPIMGFGFGLKHPPQILIKNTPVANPASTFSAKFASFITQYSTQGVSVF	479
QY	683	IFMELOKENSKNRNEVQYTSNYAASANDPVDNNGCLTEPRPICTRYLTRPL	736
Db	480	IFMELOKENSKNRNEIQYTSNYNNSVANDPVDNNGVSEBPPIDTRYLTRPL	533

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US-09-533-427-4
/ Sequence 4, Application US/09533427
/ Patent No. 6855314
/ GENERAL INFORMATION:
/ APPLICANT: Chiorini, John
/ APPLICANT: Kotlin, Robert M.
/ APPLICANT: Safer, Brian
/ APPLICANT: Davidson, Elizabeth
/ APPLICANT: Zahner, Joseph
/ FILE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
/ TITLE REFERENCE: 14014.032302
/ CURRENT APPLICATION NUMBER: US/09/533.427
/ CURRENT FILING DATE: 2000-03-22
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 724
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: /No. 6855314e =
US-09-533-427-4

Query Match          55.7%; Score 2220; DB 2; Length 724;
Best Local Similarity 58.6%; Pred. No. 5.8e-186;
Matches 431; Conservatively 81; Mismatches 198; Indels 26; Gaps 9

QY      8 PDMLIEDNISEGIRBEMWDLKPGAPKPKANQOKODDGRGLVPGYKYLGFNGLDKGPYNA 67
DB      8 PDMLIE-VQEGIRERLGLGEAGPPKPKPOQHODQAKGLVLCYNYNLGCGNGLDREGPEYNR 66
QY      68 ADAALLEHDKAYDQQLKAGDNPFYLRYNHADAFOERLOEDTSPFGNLCRAVFOAKRYLE 127
DB      67 ADEVAREHDISYNEOLEAGDNPFYLRYNHADAEFOEKLDADTSPFGNLCRAVFOAKRYLE 126
QY      128 PLGLVEGAKTAPGKKRPVEQSPQEBSSSGIGTKGQOPAKRLNLFQGTGDESVDPQOP 187
DB      127 PLGLVEGAKTAPTKRLIDHDFPKKKKART-----EEDSKP-----STSSDAEAPSGSQ 176
QY      188 LGEPPATPA-AVGPTTMAAGGAPMADNNEGADGVGNAAGNWHCDSTWLGDRVITTSRT 246
DB      177 QLOIIPAQASSISGATDTMAGGGGPGIDNNGADGVGNAAGNWHCDSTWMDGRVITTSRT 236

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```
Query Match      42.4%; Score 1690.5; DB 2; Length 544;  
Best Local Similarity 59.4%; Pctd. No. 1.3e-139;  
Matches 335; Conservative 132; Indels 25; Gaps 9  
  
QY   204 ASGGGPMADNNGAAGCVGNASGNWHDSTWLGDRTVTTSTRVWALPTYYNNHLYKQISSA 265  
| : | | | : : : | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Query Match	Similarity	Score	DB 2	Length
Best Local	58.9%	Pred. No. 2, 1e-137		
Matches	318	Conservative	54	Mismatches 154
				Gaps 5
Qy	203	MASGGCAPADNNBAGDGVGNASGNHCHSTWLGADRVITTTSTTVALPTYNHLLKQISS		26
				60
Db	1	MSAGGGGPGPDNNQGGADGVGNASGDWHCHSTWMDGVVTKSTWVLPSTNHHQYREIKS		60
Qy	263	ASTGASNDHRYFGYSTPMWGFDFNRFCHFSPPDMQRLINNNGFPRKRLNFKLNFQVK		322

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2005, 17:25:34 ; Search time 141.766 Seconds
(without alignments)
3662.868 Million cell updates/sec

Title: US-10-696-282-13
Perfect score: 3989
Sequence: 1 MAADGTLPMLEDNLSSEGIR.....NNGLYTEPRPIGTRYLTRPL 736

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query	Match	Length	DB	ID	Description
1	3989	100.0	736	2	Q9WB88	9VIRU	Q9WB88 adeno-ssoc
2	3968	99.5	736	2	Q6JC08	9VIRU	Q6JC08 adeno-ssoc
3	3963	99.3	736	2	Q56137	9VIRU	Q56137 adeno-ssoc
4	3883.5	97.4	737	2	Q6JC13	9VIRU	Q6JC13 adeno-ssoc
5	3873	97.1	736	2	Q6JC12	9VIRU	Q6JC12 adeno-ssoc
6	3853	96.6	736	2	Q6JC10	9VIRU	Q6JC10 adeno-ssoc
7	3511	88.0	736	2	Q56139	9VIRU	Q56139 adeno-ssoc
8	3494	87.6	736	2	Q65311	9VIRU	Q65311 adeno-ssoc
9	3473	87.1	736	2	Q808Y3	9VIRU	Q808Y3 non-human p
10	3469.5	87.0	735	2	Q67008	9VIRU	Q67008 adeno-ssoc
11	3456.5	86.7	735	2	Q6JB27	9VIRU	Q6JB27 adeno-ssoc
12	3456.5	86.7	737	2	Q6JC52	9VIRU	Q6JC52 adeno-ssoc
13	3455.5	86.6	737	2	Q6JC58	9VIRU	Q6JC58 adeno-ssoc
14	3453.5	86.6	735	2	Q6JC28	9VIRU	Q6JC28 adeno-ssoc
15	3453	86.6	738	2	Q6JC19	9VIRU	Q6JC19 adeno-ssoc
16	3451.5	86.5	735	2	Q6JC14	9VIRU	Q6JC14 adeno-ssoc
17	3450.5	86.5	737	2	Q6JC51	9VIRU	Q6JC51 adeno-ssoc
18	3449.5	86.5	735	2	Q6JB21	9VIRU	Q6JB21 adeno-ssoc
19	3449.5	86.5	735	2	Q6JC42	9VIRU	Q6JC42 adeno-ssoc
20	3449	86.5	738	2	Q5Y9B4	9VIRU	Q5Y9B4 adeno-ssoc
21	3449	86.5	738	2	Q6JC37	9VIRU	Q6JC37 adeno-ssoc
22	3448	86.4	738	2	Q808W5	9VIRU	Q808W5 non-human p
23	3446.5	86.4	735	2	Q6JC17	9VIRU	Q6JC17 adeno-ssoc
24	3445	86.4	738	2	Q6JC60	9VIRU	Q6JC60 adeno-ssoc
25	3443.5	86.3	737	2	Q6JC66	9VIRU	Q6JC66 adeno-ssoc
26	3442.5	86.3	735	2	Q6JC36	9VIRU	Q6JC36 adeno-ssoc
27	3442.5	86.3	737	2	Q8JCG0	9VIRU	Q8JCG0 adeno-ssoc
28	3442	86.3	738	2	Q6JC14	9VIRU	Q6JC14 adeno-ssoc
29	3442	86.3	738	2	Q6JC56	9VIRU	Q6JC56 adeno-ssoc
30	3441.5	86.3	735	2	Q6JC44	9VIRU	Q6JC44 adeno-ssoc
31	3440	86.2	738	2	Q6JC15	9VIRU	Q6JC15 adeno-ssoc

32	3440	86.2	738	2	Q6JC16	9VIRU	Q6JC16 adeno-ssoc
33	3440	86.2	738	2	Q6JC62	9VIRU	Q6JC62 adeno-ssoc
34	3439	86.2	738	2	Q6JB22	9VIRU	Q6JB22 adeno-ssoc
35	3438	86.2	734	2	Q6JC02	9VIRU	Q6JC02 adeno-ssoc
36	3438	86.2	738	2	Q808X3	9VIRU	Q808X3 non-human p
37	3437	86.2	738	2	Q6JC47	9VIRU	Q6JC47 adeno-ssoc
38	3437	86.2	738	2	Q6JC61	9VIRU	Q6JC61 adeno-ssoc
39	3436	86.1	734	2	Q6JC04	9VIRU	Q6JC04 adeno-ssoc
40	3434.5	86.1	735	2	Q6JB26	9VIRU	Q6JB26 adeno-ssoc
41	3434	86.1	728	2	Q808X4	9VIRU	Q808X4 non-human p
42	3434	86.1	738	2	Q6JB23	9VIRU	Q6JB23 adeno-ssoc
43	3433	86.1	738	2	Q6JC49	9VIRU	Q6JC49 adeno-ssoc
44	3433	86.1	738	2	Q6JC53	9VIRU	Q6JC53 adeno-ssoc
45	3432	86.0	738	2	Q6JC54	9VIRU	Q6JC54 adeno-ssoc

ALIGNMENTS

RESULT 1
Q9WB88_9VIRU PRELIMINARY; PRT; 736 AA.
AC Q9WB88;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Capsid protein.
OS Adeno-associated virus 1.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=85106;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9214338; PubMed=10196295;
RA Xiao W., Chirmule N., Barta S.C., McCullough B., Gao G., Wilson J.M.;
RT "Gene therapy vectors based on adeno-associated virus type 1.";
RL J. Virol. 73:3994-4003(1999).
EMBL: AF063497; AM22757.1; -; Genomic_DNA.
DR SMR; Q9WB88; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo coat.
DR Pfam; PF00740; Parvo coat; 1.
SQ SEQUENCE 736 AA; 81375 MW; CFAFB9BDSCD0595 CRC64;

Query Match 100.0%; Score 3989; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.1e-249;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAADGTLPMLEDNLSSEGIR	WMDLKRGA	PKRANQKDDGGLVPGKYLGPPNGLD	60
DB	1	MAADGTLPMLEDNLSSEGIR	WMDLKRGA	PKRANQKDDGGLVPGKYLGPPNGLD	60
QY	61	KCEPVAAADAALEHDKAVDQOLKAGDNPYLKRNHDAFEQERLOEDTFFGNGLGRAVQ			120
DB	61	KCEPVAAADAALEHDKAVDQOLKAGDNPYLKRNHDAFEQERLOEDTFFGNGLGRAVQ			120
QY	121	AKKRVLEPLGLVEEGAKTAPGKKRPVQSGPOEBSSSGIGKTGQOPAKKRLNFGQTGDS			180
DB	121	AKKRVLEPLGLVEEGAKTAPGKKRPVQSGPOEBSSSGIGKTGQOPAKKRLNFGQTGDS			180
QY	181	SVDPDPLGEPATPAVAGPTTMASSGGA	PMADNNGACGCVGASGNMHCDSITWLDGRI		240
DB	181	SVDPDPLGEPATPAVAGPTTMASSGGA	PMADNNGACGCVGASGNMHCDSITWLDGRI		240
QY	241	TTSTRTMALPTYNNHLKXOISSASTGASNDNHYFGYSTPMGVPDFNRFHCFSPRDMQRL			300
DB	241	TTSTRTMALPTYNNHLKXOISSASTGASNDNHYFGYSTPMGVPDFNRFHCFSPRDMQRL			300
QY	301	INNMGFRPRRLNFKLNFIVKEVTTNDGVTIANNLSTTVQYFSDSEYQLPYVLSAQH			360
DB	301	INNMGFRPRRLNFKLNFIVKEVTTNDGVTIANNLSTTVQYFSDSEYQLPYVLSAQH			360
QY	361	GCLPPPADVFMIPQYGYLTINNGSQAVGRSSRYCLEFPSSQLRIGNNTFTFYTEEVP			420

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Db 361 GCLPPADVFMIPQGYLTLLNNGSAVGRSSFYCLEYFPBQMLRTGNNFTFSYTFEEVP 420
Qy 421 FHSYASHQSIDRLMNPILIDQYLYLNTQONSSAQNKDLIFSRGSPAGMSVQPKMLP 480
Db 421 FHSYASHQSIDRLMNPILIDQYLYLNTQONSSAQNKDLIFSRGSPAGMSVQPKMLP 480
Qy 481 GPCYRQGVSKTKTDNNNSNFTWGASKYNLNGRESIINPGTAMASHKODEDKFFPMSCV 540
Db 481 GPCYRQGVSKTKTDNNNSNFTWGASKYNLNGRESIINPGTAMASHKODEDKFFPMSCV 540
Qy 541 MIFGESAGASNTALDNVMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGDVHAMG 600
Db 541 MIFGESAGASNTALDNVMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGDVHAMG 600
Qy 601 ALPGWVQDRDVLVYLGPIWAKIPHTDGHFHSPLMGSGGLKNPPQILLIKTVPANPPA 660
Db 601 ALPGWVQDRDVLVYLGPIWAKIPHTDGHFHSPLMGSGGLKNPPQILLIKTVPANPPA 660
Qy 661 EFSATKFPASFTQYSTGVSVIEIEMELQENSKRNPEVOYTSNYAKSANDFTVDNGL 720
Db 661 EFSATKFPASFTQYSTGVSVIEIEMELQENSKRNPEVOYTSNYAKSANDFTVDNGL 720
Qy 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736

RESULT 2
06JUC08 9VIRU PRELIMINARY; PRT; 736 AA.
AC 06JUC08
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Capsid protein VPI.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Dependovirus.
OC NCBI_TaxId=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvirra M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL: AY530611; AAS99296.1; -; Genomic_DNA.
DR SMR: 06JUC08; 217-736.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo_coat.
DR Pfam: PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD CRC64;

Query Match 99.5%; Score 3968; DB 2; Length 736;
Best Local Similarity 99.3%; Pred. No. 2,6e-248;
Matches 731; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Db 181 SVDPQGLGEPPTAAVGTPTMASGGA PMADNNEGADVGNAAGNMHCSTWLGDRI 240
Qy 241 TTSRTALPTYNHLLYKQISSASTGASNDNHVGYSTPMGYPDPFNFFHCFSPRDMQRL 300
Db 241 TTSRTALPTYNHLLYKQISSASTGASNDNHVGYSTPMGYPDPFNFFHCFSPRDMQRL 300
Qy 301 INNMGRPKRLNKLNIQVEYTTNDGVTTLANNLTSTVQVSDSEYQLPYLGSAHQ 360
Db 301 INNMGRPKRLNKLNIQVEYTTNDGVTTLANNLTSTVQVSDSEYQLPYLGSAHQ 360
Qy 361 GCLPPADVFMIPQGYLTLLNNGSAVGRSSFYCLEYFPBQMLRTGNNFTFSYTFEEVP 420
Db 361 GCLPPADVFMIPQGYLTLLNNGSAVGRSSFYCLEYFPBQMLRTGNNFTFSYTFEEVP 420
Qy 421 FHSYASHQSIDRLMNPILIDQYLYLNTQONSSAQNKDLIFSRGSPAGMSVQPKMLP 480
Db 421 FHSYASHQSIDRLMNPILIDQYLYLNTQONSSAQNKDLIFSRGSPAGMSVQPKMLP 480
Qy 481 GPCYRQGVSKTKTDNNNSNFTWGASKYNLNGRESIINPGTAMASHKODEDKFFPMSCV 540
Db 481 GPCYRQGVSKTKTDNNNSNFTWGASKYNLNGRESIINPGTAMASHKODEDKFFPMSCV 540
Qy 541 MIFGESAGASNTALDNVMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGDVHAMG 600
Db 541 MIFGESAGASNTALDNVMTDEBEIKATNPATERFGTVAVNFQSSSTDPAIGDVHAMG 600
Qy 601 ALPGWVQDRDVLVYLGPIWAKIPHTDGHFHSPLMGSGGLKNPPQILLIKTVPANPPA 660
Db 601 ALPGWVQDRDVLVYLGPIWAKIPHTDGHFHSPLMGSGGLKNPPQILLIKTVPANPPA 660
Qy 661 EFSATKFPASFTQYSTGVSVIEIEMELQENSKRNPEVOYTSNYAKSANDFTVDNGL 720
Db 661 EFSATKFPASFTQYSTGVSVIEIEMELQENSKRNPEVOYTSNYAKSANDFTVDNGL 720
Qy 721 YTEPRPIGTRYLTRPL 736
Db 721 YTEPRPIGTRYLTRPL 736

RESULT 3
056137 9VIRU PRELIMINARY; PRT; 736 AA.
ID 056137 9VIRU PRELIMINARY;
AC 056137
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Capsid protein VPI.
OS Adeno-associated virus 6.
OC Viruses; ssDNA viruses; Parvoviridae; Dependovirus.
OC NCBI_TaxId=68558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE:98080418; PubMed:9420229;
RA Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2.";
RL J. Virol. 72:309-319(1998).
DR EMBL: AF028704; AAB95450.1; -; Genomic_DNA.
DR SMR: 056137; 217-736.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo_coat.
DR Pfam: PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81411 MW; 311217A089C565F5 CRC64;

Query Match 99.3%; Score 3963; DB 2; Length 736;
Best Local Similarity 99.2%; Pred. No. 5,4e-248;
Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 61 KSEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADADEFQERLQEDTSPFGNLGRAVQ 120
DB 61 KSEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADADEFQERLQEDTSPFGNLGRAVQ 120
QY 121 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGTKGQOPAKKRLNFGQDSE 180
DB 121 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGTKGQOPAKKRLNFGQDSE 180
QY 181 SVDPDPLGEPAPATPAVGPPTTMASSGGA PMADNNBGADGVGNASGNWCHDSTWLGDYI 240
DB 181 SVDPDPLGEPAPATPAVGPPTTMASSGGA PMADNNBGADGVGNASGNWCHDSTWLGDYI 240
QY 241 TTSTRTALPTYNNHLKYQISSASTGASNDNHFGYSTPWGYFDPNRPHCHSPRDWQR 300
DB 241 TTSTRTALPTYNNHLKYQISSASTGASNDNHFGYSTPWGYFDPNRPHCHSPRDWQR 300
QY 301 INNMGFRPKRLNFKLFNIQVKEVTNDGVTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
DB 301 INNMGFRPKRLNFKLFNIQVKEVTNDGVTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
QY 361 GCLPPPADVPMIPOGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYTFEEYV 420
DB 361 GCLPPPADVPMIPOGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYTFEEYV 420
QY 421 FHSSYAHOSQSLDRMLNPLIDQYLTYLNRTONOGSAQNKDILFSGSPAGMSVQPKWLP 480
DB 421 FHSSYAHOSQSLDRMLNPLIDQYLTYLNRTONOGSAQNKDILFSGSPAGMSVQPKWLP 480
QY 481 GPCYRQORVSKTIDNNNSNFTWTGASKYLNLRGSIINFGTMAASHKDEDEKFFPMGCV 540
DB 481 GPCYRQORVSKTIDNNNSNFTWTGASKYLNLRGSIINFGTMAASHKDEDEKFFPMGCV 540
QY 541 MIFGKESAGASNTALDNMTDEEBEIKATNPVATERFGTVAVNFOSSSTDPAATGVHAM 600
DB 541 MIFGKESAGASNTALDNMTDEEBEIKATNPVATERFGTVAVNFOSSSTDPAATGVHAM 600
QY 601 ALPGMWODRDVYLOGPIWAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTVPVANPP 660
DB 601 ALPGMWODRDVYLOGPIWAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTVPVANPP 660
QY 661 EBSATKPAFTTQYSTGVSEIEMELQKENSKRANPEVQYTSNYAKSANVDTVDNNG 720
DB 661 EBSATKPAFTTQYSTGVSEIEMELQKENSKRANPEVQYTSNYAKSANVDTVDNNG 720
QY 721 YTEPRPIGTRYLTRPL 736
DB 721 YTEPRPIGTRYLTRPL 736

DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo Coat.
DR Pfam: PF00740; Parvo Coat; 1.
DR SEQUENCE 737 AA; 81332 MW; 94CED0F3AFD6E492 CRC64;
Query Match 97.4%; Score 3883.5; DB 2; Length 737;
Best Local Similarity 97.4%; Pred. No. 7.7e-243;
Matches 718; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
QY 1 MAADGYLPDWEEDNLSEGIREWMDLKPAGPKKANQOKDDGRGLVPGYKYLGPENGLD 60
DB 1 MAADGYLPDWEEDNLSEGIREWMDLKPAGPKKANQOKDDGRGLVPGYKYLGPENGLD 60
QY 61 KSEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADADEFQERLQEDTSPFGNLGRAVQ 120
DB 61 KSEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADADEFQERLQEDTSPFGNLGRAVQ 120
QY 121 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGTKGQOPAKKRLNFGQDGS 179
DB 121 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQSPDSTGIGKKGQOPAKKRLNFGQDGS 180
QY 180 ESVDPDPLGEPAPATPAVGPPTTMASSGGA PMADNNBGADGVGNASGNWCHDSTWLGDYI 239
DB 181 ESVDPDPLGEPAPATPAVGPPTTMASSGGA PMADNNBGADGVGNASGNWCHDSTWLGDYI 240
QY 240 TTSTRTALPTYNNHLKYQISSASTGASNDNHFGYSTPWGYFDPNRPHCHSPRDWQR 239
DB 241 TTSTRTALPTYNNHLKYQISSASTGASNDNHFGYSTPWGYFDPNRPHCHSPRDWQR 300
QY 300 LNNMGFRPKRLNFKLFNIQVKEVTNDGVTIANNLSTVQVFSDEYQLPYVLGSAHQ 359
DB 301 LNNMGFRPKRLNFKLFNIQVKEVTNDGVTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
QY 360 GCLPPPADVPMIPOGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYTFEEYV 419
DB 361 GCLPPPADVPMIPOGYLTLLNGSOAVGRSSFYCLEYFPSSQMLRTGNNFTFSYTFEEYV 420
QY 420 FHSSYAHOSQSLDRMLNPLIDQYLTYLNRTONOGSAQNKDILFSGSPAGMSVQPKWLP 479
DB 421 FHSSYAHOSQSLDRMLNPLIDQYLTYLNRTONOGSAQNKDILFSGSPAGMSVQPKWLP 480
QY 480 GPCYRQORVSKTIDNNNSNFTWTGASKYLNLRGSIINFGTMAASHKDEDEKFFPMGCV 539
DB 481 GPCYRQORVSKTIDNNNSNFTWTGASKYLNLRGSIINFGTMAASHKDEDEKFFPMGCV 540
QY 540 VMIFGKESAGASNTALDNMTDEEBEIKATNPVATERFGTVAVNFOSSSTDPAATGVHAM 539
DB 541 VMIFGKESAGASNTALDNMTDEEBEIKATNPVATERFGTVAVNFOSSSTDPAATGVHAM 600
QY 600 GALPGMWODRDVYLOGPIWAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTVPVANPP 659
DB 601 GALPGMWODRDVYLOGPIWAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTVPVANPP 660
QY 660 AEFSAKPAFTTQYSTGVSEIEMELQKENSKRANPEVQYTSNYAKSANVDTVDNNG 719
DB 661 AEFSAKPAFTTQYSTGVSEIEMELQKENSKRANPEVQYTSNYAKSANVDTVDNNG 720
QY 720 LYTEPRPIGTRYLTRPL 736
DB 721 LYTEPRPIGTRYLTRPL 737

RESULT 4
Q6JC13_9VIRU PRT; 737 AA.
AC Q6JC13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
NCBI_Taxid=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues".
RL J. Virol. 78:6381-6388(2004).
DR EMBL, AY530606; AAS99291.1; -, Genomic_DNA.
DR SMR; Q6JC13; 218-737.
DR GO; GO:0019028; C:viral capsid; IEA.

RESULT 5
Q6JC12_9VIRU PRT; 736 AA.
AC Q6JC12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.

OX NCBI_TaxID=272636;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RX Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues";
RL J. Virol. 78:6381-6388(2004).
DR EMBL: AY530607; AAS9292.1; -; Genomic_DNA.
DR SMR: Q6JC12; 217-736.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo coat.
DR Pfam: PF00740; Parvo coat; 1.
SQ SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CRC64;

Query Match 97.1%; Score 3873; DB 2; Length 736;
Best Local Similarity 96.9%; Pred. No. 3.7e-242;
Matches 713; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MAADGVLPMLENDLSEGRREWDLKPGAPRKANQKODDGRGLVLEGYKTLGPFNGLD 60
DB 1 MAADGVLPMLENDLSEGRREWDLKPGAPRKANQKODDGRGLVLEGYKTLGPFNGLD 60
QY 61 KGEFVNADAAALSHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSFGNIGRAVFQ 120
DB 61 KGEFVNADAAALSHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSFGNIGRAVFQ 120
QY 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTQOQPAKKRLNFGQTGSE 180
DB 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTQOQPAKKRLNFGQTGSE 180
QY 181 SVDPQPLGEPAPATPAAGPTTMAAGGAPADNNEGADGVNAGNHCSTWLGDVYI 240
DB 181 SVDPQPLGEPAPATPAAGPTTMAAGGAPADNNEGADGVNAGNHCSTWLGDVYI 240
QY 241 TTSTRTMLPTVNNHLYKQISSASTGASNDNHFGYSTPMGFDFNRFCHFSPPDMQRL 300
DB 241 TTSTRTMLPTVNNHLYKQISSASTGASNDNHFGYSTPMGFDFNRFCHFSPPDMQRL 300
QY 301 INNNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
DB 301 INNNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
QY 361 GCLPPFPADVPMIPOYGYLTLLNGSQAAGRSSFYCLEYFPQMLRTGNFTFSYFEEVP 420
DB 361 GCLPPFPADVPMIPOYGYLTLLNGSQAAGRSSFYCLEYFPQMLRTGNFTFSYFEEVP 420
QY 421 FHSSTAHQSOSLDRLNMPLIIDQYLYLNTQNGSQAOKDILFSRGSPPAGMSVOPKMWLP 480
DB 421 FHSSTAHQSOSLDRLNMPLIIDQYLYLNTQNGSQAOKDILFSRGSPPAGMSVOPKMWLP 480
QY 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRSSIINPGTAMASHKODEDKFPFMGCV 540
DB 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRSSIINPGTAMASHKODEDKFPFMGCV 540
QY 541 MIFGKESAGASNTALDNVMTIDBEERIKATNPVATERFGTVAVNFGSSSTDPAIGVHAMG 600
DB 541 MIFGKESAGASNTALDNVMTIDBEERIKATNPVATERFGTVAVNFGSSSTDPAIGVHAMG 600
QY 601 ALPGWVQORVDVYLQOPIWAKIPIHTDGHFHPSPILMGFGILKNPPOILIKNTPVANPAP 660
DB 601 ALPGWVQORVDVYLQOPIWAKIPIHTDGHFHPSPILMGFGILKNPPOILIKNTPVANPAP 660
QY 661 EFSATKFAAFITQYSTGVSVLEIEMELQKENSKRNPPEVQYTSNKAASANVDFYDNGGL 720
DB 661 EFSATKFAAFITQYSTGVSVLEIEMELQKENSKRNPPEVQYTSNKAASANVDFYDNGGL 720
QY 721 YTEPRPIGTRYLTRPL 736
DB 721 YTEPRPIGTRYLTRPL 736

RESULT 6
06JC10_VIRU
ID 06JC10_VIRU PRELIMINARY; PRT; 736 AA.
AC 06JC10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Capsid protein VP1.
CN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues";
RL J. Virol. 78:6381-6388(2004).
DR EMBL: AY530609; AAS9294.1; -; Genomic_DNA.
DR SMR: Q6JC10; 217-736.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo coat.
DR Pfam: PF00740; Parvo coat; 1.
SQ SEQUENCE 736 AA; 81388 MW; BA9463E970028DFO CRC64;

Query Match 96.6%; Score 3853; DB 2; Length 736;
Best Local Similarity 96.6%; Pred. No. 7.3e-241;
Matches 711; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAADGVLPMLENDLSEGRREWDLKPGAPRKANQKODDGRGLVLEGYKTLGPFNGLD 60
DB 1 MAADGVLPMLENDLSEGRREWDLKPGAPRKANQKODDGRGLVLEGYKTLGPFNGLD 60
QY 61 KGEFVNADAAALSHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSFGNIGRAVFQ 120
DB 61 KGEFVNADAAALSHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSFGNIGRAVFQ 120
QY 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTQOQPAKKRLNFGQTGSE 180
DB 121 AKKRVLEPLGLVEBGAKTAPGKKRPVEQSPQEPDSSSGIGKTQOQPAKKRLNFGQTGSE 180
QY 181 SVDPQPLGEPAPATPAAGPTTMAAGGAPADNNEGADGVNAGNHCSTWLGDVYI 240
DB 181 SVDPQPLGEPAPATPAAGPTTMAAGGAPADNNEGADGVNAGNHCSTWLGDVYI 240
QY 241 TTSTRTMLPTVNNHLYKQISSASTGASNDNHFGYSTPMGFDFNRFCHFSPPDMQRL 300
DB 241 TTSTRTMLPTVNNHLYKQISSASTGASNDNHFGYSTPMGFDFNRFCHFSPPDMQRL 300
QY 301 INNNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
DB 301 INNNMGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQ 360
QY 361 GCLPPFPADVPMIPOYGYLTLLNGSQAAGRSSFYCLEYFPQMLRTGNFTFSYFEEVP 420
DB 361 GCLPPFPADVPMIPOYGYLTLLNGSQAAGRSSFYCLEYFPQMLRTGNFTFSYFEEVP 420
QY 421 FHSSTAHQSOSLDRLNMPLIIDQYLYLNTQNGSQAOKDILFSRGSPPAGMSVOPKMWLP 480
DB 421 FHSSTAHQSOSLDRLNMPLIIDQYLYLNTQNGSQAOKDILFSRGSPPAGMSVOPKMWLP 480
QY 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRSSIINPGTAMASHKODEDKFPFMGCV 540
DB 481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRSSIINPGTAMASHKODEDKFPFMGCV 540
QY 541 MIFGKESAGASNTALDNVMTIDBEERIKATNPVATERFGTVAVNFGSSSTDPAIGVHAMG 600
DB 541 MIFGKESAGASNTALDNVMTIDBEERIKATNPVATERFGTVAVNFGSSSTDPAIGVHAMG 600

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QY 601 ALPGWVQDRDVLVYLCGPIMAKI PHTDGHFHSPLMGFGKLNPPPOILLKNTVPANPPA 660
DB 601 ALPGWVQDRDVLVYLCGPIMAKI PHTDGHFHSPLMGFGKLNPPPOILLKNTVPANPPA 660
QY 661 EESATKFAFPIYQSTGQSVVEIEMELCKENSKRMNBEVQYTSNYSKANSANVDFYDNNGL 720
DB 661 EESATKFAFPIYQSTGQSVVEIEMELCKENSKRMNBEVQYTSNYSKANSANVDFYDNNGL 720
QY 721 YTEPRPIGTRVLTPL 736
DB 721 YTEPRPIGTRVLTPL 736

RESULT 7
056139_9VIRU PRELIMINARY; PRT: 736 AA.
ID 056139_9VIRU PRELIMINARY; PRT: 736 AA.
AC 056139;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein VPI.
OS Adeno-associated virus 3B.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=68742;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=98080418; PubMed=9420229;
RX Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2."
RL J. Virol. 72:309-319(1998).
DR EMBL; AF028705; AAB95452.1; -; Genomic_DNA.
DR SMR; 056139; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81906 MW; DD52331AD5FD070F CRC64;

Query Match 88.0%; Score 3511; DB 2; Length 736;
Best Local Similarity 86.4%; Pred. No. 1e-216;
Matches 640; Conservative 38; Mismatches 57; Indels 2; Gaps 2;
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DB 420 FHSYAHQSLSRLMNPILDOYLYLNRTQGTSTGNQSRLLFSQAGPQSMQLQARWL 479
QY 480 PGPCTROQRVSKTQDNNNSNFTGASKNLNGEBSIINPTAAASHKDDDKFFPMSC 539
DB 480 PGPCTROQRLSTKXANDNNNSNFPMTAASKYHLNGRDSLVNPGPAAASHDDDEKFFPMSC 539
QY 540 VMIPKESAGSNTLADVMITDEEIKATNPVATEREGTVAVNFOSSSTDPAQDVHAM 599
DB 540 NLIFFEGETTASNAEDVMITDEEIKATNPVATEREGTVAVNFOSSSTDPAQDVHAM 599
QY 600 GALPGWVQDRDVLVYLCGPIMAKI PHTDGHFHSPLMGFGKLNPPPOILLKNTVPANPP 659
DB 600 GALPGWVQDRDVLVYLCGPIMAKI PHTDGHFHSPLMGFGKLNPPPOILLKNTVPANPP 659
QY 660 AEFSAKFAFPIYQSTGQSVVEIEMELCKENSKRMNBEVQYTSNYSKANSANVDFYDNNNG 719
DB 660 TTFSPAKFAFPIYQSTGQSVVEIEMELCKENSKRMNBEIQTYSNYSKANSANVDFYDNNNG 719
QY 720 LYTEPRPIGTRVLTPL 736
DB 720 YTEPRPIGTRVLTPL 736

RESULT 8
065311_9VIRU PRELIMINARY; PRT: 736 AA.
ID 065311_9VIRU PRELIMINARY; PRT: 736 AA.
AC 065311;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein.
OS Adeno-associated virus 3.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=46350;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=96266430; PubMed=8661429; DOI=10.1006/viro.1996.0367;
RX Murakatsu S., Mizukami H., Young N.S., Brown K.B.;
RT "Nucleotide sequencing and generation of an infectious clone of adeno-
RT associated virus 3."
RL Virology 221:208-217(1996).
DR EMBL; U48704; AAC55049.1; -; Genomic_DNA.
DR SMR; 065311; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81660 MW; APTLEF47B5C67A10 CRC64;

Query Match 87.6%; Score 3494; DB 2; Length 736;
Best Local Similarity 86.4%; Pred. No. 1.3e-217;
Matches 637; Conservative 39; Mismatches 59; Indels 2; Gaps 2;
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Oy 301 INNMGFRPKRLNFKLFIQVKEVTTNDGVTTIANNLSTVQVFSDESEYQLPYVLGSAHQ 360
Db 300 INNMGFRPKLSFLKLFNIQVKGVTQNDGTTIANNLSTVQVFTDSRYQLPYVLGSAHQ 359
Oy 361 GCLPPPADVPMIPOYGYLLTLNNGSAVGRSSFYCLEYFPQOMLRTGNNFTFSYTFEEVP 420
Db 360 GCLPPPADVPMVPOYGYLLTLNNGSAVGRSSFYCLEYFPQOMLRTGNNFTFSYTFEEVP 419
Oy 421 FHSSVAHSQSILDRMLNPLIDQYLYLNRTO-NQSSAQNKLIFSRGSPAGMSVQPKMWL 479
Db 420 FHSSVAHSQSILDRMLNPLIDQYLYLNRTO-NQSSAQNKLIFSRGSPAGMSVQPKMWL 479
Oy 480 PGPCYRQORVSKTKTDNNNSNFTWTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMG 539
Db 480 PGPCYRQORVSKTKTDNNNSNFTWTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMG 539
Oy 540 VMIPEKESAGASNTALDNVMTDEEBEIKATNPVATERPGTVAVNFQSSSTDPAIGDVHAM 599
Db 540 VMIPEKESAGASNTALDNVMTDEEBEIKATNPVATERPGTVAVNFQSSSTDPAIGDVHAM 599
Oy 600 GALPGMWODRDVYLOGPIMAKIPHTDGHFHSPLMGFGKLNPPOLLIKXTVPVPAWP 659
Db 600 GALPGMWODRDVYLOGPIMAKIPHTDGHFHSPLMGFGKLNPPOLLIKXTVPVPAWP 659
Oy 660 AEFSAATKFASTITQYSTQGVSEIEMELOKENSXKMNPEVOYTSNVAKSANVDFTVDNNG 719
Db 660 TTFSAKPAKPSFTITQYSTQGVSEIEMELOKENSXKMNPEVOYTSNVAKSANVDFTVDNNG 719
Oy 720 LYTEPRPIGTRYLTRPL 736
Db 720 VYSEPRPIGTRYLTRNL 736

RESULT 9
ID Q808Y3_9VIRU PRELIMINARY; PRT; 736 AA.
AC Q808Y3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Capsid protein.
GN Name=VPI;
OS Non-human primate Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
CX NCBI_TaxID=226582;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22631657; PubMed=12716974; DOI=10.1073/pnas.0937739100;
RA Gao G., Alvirra M.R., Somanathan S., Lu Y., Vandenbergh L.H.,
RT "Adeno-associated viruses undergo substantial evolution in primates
RT during natural infections."
RT Proc. Natl. Acad. Sci. U.S.A. 100:6081-6086(2003).
DR EMBL; AY242997; AA088183.1; -; Genomic_DNA.
DR SMR; Q808Y3; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat.1.
SQ SEQUENCE 736 AA; 81370 MW; 87D05047F8FA14C CRC64;

Query Match 87.1%; Score 3473; DB 2; Length 736;
Best Local Similarity 85.6%; Pred. No. 3e-216;
Matches 631; Conservative 44; Mismatches 60; Indels 2; Gaps 2;

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Oy 121 AKKVLBPLGVEGAKTAPDKKRPVEQSPQEPSSSGIGTKGQAPAKKRLNFGQTDSE 180
Db 121 AKKVLBPLGVEGAKTAPDKKRPVEQSPQEPSSSGIGTKGQAPAKKRLNFGQTDSE 180
Oy 181 SVDPQPLGEPATPAVAVPTTMAAGCAADANNBAGADGVNAGSMWCHDSITMLGDRVI 240
Db 181 SVDPQPLGEPATPAVAVPTTMAAGCAADANNBAGADGVNAGSMWCHDSITMLGDRVI 240
Oy 241 TTSRTMALPTYNHLLKQIISASGTAS-NDNHFGSTDMGVDNFNRPHCFSPRDMOR 299
Db 241 TTSRTMALPTYNHLLKQIISASGTAS-NDNHFGSTDMGVDNFNRPHCFSPRDMOR 299
Oy 300 LINNMGFRPKRLNFKLFIQVKEVTTNDGVTTIANNLSTVQVFSDESEYQLPYVLGSAH 359
Db 301 LINNMGFRPKRLNFKLFIQVKEVTTNDGVTTIANNLSTVQVFTDSRYQLPYVLGSAH 360
Oy 360 GCLPPPADVPMIPOYGYLLTLNNGSAVGRSSFYCLEYFPQOMLRTGNNFTFSYTFEEV 419
Db 361 GCLPPPADVPMVPOYGYLLTLNNGSAVGRSSFYCLEYFPQOMLRTGNNFTFSYTFEEV 420
Oy 420 PFHSSVAHSQSILDRMLNPLIDQYLYLNRTO-NQSSAQNKLIFSRGSPAGMSVQPKMWL 479
Db 421 PFHSSVAHSQSILDRMLNPLIDQYLYLNRTO-TGTGCTQLASQAGPSSMAAQARNV 479
Oy 480 PGPCYRQORVSKTKTDNNNSNFTWTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMG 539
Db 480 PGPCYRQORVSKTKTDNNNSNFTWTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMG 539
Oy 540 VMIPEKESAGASNTALDNVMTDEEBEIKATNPVATERPGTVAVNFQSSSTDPAIGDVHAM 599
Db 540 VMIPEKESAGASNTALDNVMTDEEBEIKATNPVATERPGTVAVNFQSSSTDPAIGDVHAM 599
Oy 600 GALPGMWODRDVYLOGPIMAKIPHTDGHFHSPLMGFGKLNPPOLLIKXTVPVPAWP 659
Db 600 GALPGMWODRDVYLOGPIMAKIPHTDGHFHSPLMGFGKLNPPOLLIKXTVPVPAWP 659
Oy 660 AEFSAATKFASTITQYSTQGVSEIEMELOKENSXKMNPEVOYTSNVAKSANVDFTVDNNG 719
Db 660 LTFNQAALNSFTITQYSTQGVSEIEMELOKENSXKMNPEVOYTSNVAKSANVDFTVDNNG 719
Oy 720 LYTEPRPIGTRYLTRPL 736
Db 720 VYSEPRPIGTRYLTRNL 736

RESULT 10
ID Q670Q8_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q670Q8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Capsid protein VPI.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
CX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chen C.L., Jensen R.L., Schnepf B.C., Connell M.J., Bartlett J.S.,
RT "Characterization of Adeno-Associated Viruses in Children."
RT Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY695376; AAU05370.1; -; Genomic_DNA.
DR SMR; Q670Q8; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat.1.
SQ SEQUENCE 735 AA; 81867 MW; 258BF955F1C9925 CRC64;

Query Match 87.0%; Score 3469.5; DB 2; Length 735;

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Best Local Similarity 85.1%; Pred. No. 5e-216; Matches 626; Conservative 47; Mismatches 62; Indels 1; Gaps 1;

QY 1 MAADGYPDWLEDNISEGIREWMWLKPGAPKPKANQKODDGRGLVPGYKYLGFPGNGID 60
DB 1 MAADGYPDWLEDNISEGIREWMWLKPGAPKPKPKRPRKRAHRHDDRGVLPGYKYLGFPGNGID 60
QY 61 KCEPVNAADAAALHDKAYDQOLKAGDNPYLRYNHADADEFORLLOEDTSFGGNLGRAVQ 120
DB 61 KCEPVNAADAAALHDKAYDQOLKAGDNPYLRYNHADADEFORLLOEDTSFGGNLGRAVQ 120
QY 121 AKKRVLEPGLVEEGAKTAPGKKRPVEOSPOBDSGGIGKTGQOQPAKKRLNFGQTGDS 180
DB 121 AKKRVLEPGLVEEGAKTAPGKKRPVEOSPOBDSGGIGKTGQOQPAKKRLNFGQTGDS 180
QY 181 SVDPDQPLGEPPTPAVGPPTTMASSGGA PMADNNEGADVGNASGNHCDSTWLGDRVI 240
DB 181 SVDPDQPLGEPPTPAVGPPTTMASSGGA PMADNNEGADVGNASGNHCDSTWLGDRVI 240
QY 241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHFGYSTPWGYPDFNRFFCHSPRDWQRL 300
DB 241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHFGYSTPWGYPDFNRFFCHSPRDWQRL 299
QY 301 INNNNGEPRKRLNFKLFTNIOVEKVTNDGVTIANNLSTVOYFSDSEYQLPYVLGSAHQ 360
DB 301 INNNNGEPRKRLNFKLFTNIOVEKVTNDGVTIANNLSTVOYFSDSEYQLPYVLGSAHQ 359
QY 361 GCLPPPADVFMIPQYGYLTNNGSAVGRSSFCLEYPSSQMLRTGNNFTFSYTEEVP 420
DB 361 GCLPPPADVFMIPQYGYLTNNGSAVGRSSFCLEYPSSQMLRTGNNFTFSYTEEVP 419
QY 421 FHSSTYAHQSGLRLMNP.LIDQYLYLNRTONOGSAONKDLFSRGS PAMGSAVQPNWLP 480
DB 421 FHSSTYAHQSGLRLMNP.LIDQYLYLNRTONOGSAONKDLFSRGS PAMGSAVQPNWLP 479
QY 481 GPCYRQORVSKTKTNNNSNFTTGASKYNLGRBSI INPGTAMASHKXDEDEKFFPMGCV 540
DB 481 GPCYRQORVSKTKTNNNSNFTTGASKYNLGRBSI INPGTAMASHKXDEDEKFFPMGCV 539
QY 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFGTVAVNFOSSTDPATGDVHANG 600
DB 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFGTVAVNFOSSTDPATGDVHANG 599
QY 601 ALPGMWQDRDYLQGPIMAKI.PHTDGHFHPSPLMGFGGLKNPPOILLKNTFVPANPRA 660
DB 601 ALPGMWQDRDYLQGPIMAKI.PHTDGHFHPSPLMGFGGLKNPPOILLKNTFVPANPRA 659
QY 661 EFSATKFAFTIOYSTGOVSVEIEMELQKENSXKRNPEVOYTSNYAKSANVDTVDNGL 720
DB 661 EFSATKFAFTIOYSTGOVSVEIEMELQKENSXKRNPEVOYTSNYAKSANVDTVDNGL 719
QY 721 YTEPRPIGTRYLTRPL 736
DB 721 YTEPRPIGTRYLTRPL 735

RESULT 11
Q6JB27_9VIRU
ID Q6JB27_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JB27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
ON NCBI_TaxID=272636;
RX PubMed=15163731, DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X., Wilson J.M.;

RT "Clades of Adeno-associated viruses are widely disseminated in human tissues.";
RT U. Virol. 78:6381-6388(2004).
DR EMBL; AY530622; AAS99307.1; -; Genomic_DNA.
DR SMR; Q6JB27; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parv_coat.
DR Pfam; PF00740; Parv_coat; 1.
SQ SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A CRC64;

Query Match 86.7%; Score 3456.5; DB 2; Length 735;
Best Local Similarity 84.5%; Pred. No. 3.5e-215;
Matches 622; Conservative 49; Mismatches 64; Indels 1; Gaps 1;

QY 1 MAADGYPDWLEDNISEGIREWMWLKPGAPKPKANQKODDGRGLVPGYKYLGFPGNGID 60
DB 1 MAADGYPDWLEDNISEGIREWMWLKPGAPKPKPKRPRKRAHRHDDRGVLPGYKYLGFPGNGID 60
QY 61 KCEPVNAADAAALHDKAYDQOLKAGDNPYLRYNHADADEFORLLOEDTSFGGNLGRAVQ 120
DB 61 KCEPVNAADAAALHDKAYDQOLKAGDNPYLRYNHADADEFORLLOEDTSFGGNLGRAVQ 120
QY 121 AKKRVLEPGLVEEGAKTAPGKKRPVEOSPOBDSGGIGKTGQOQPAKKRLNFGQTGDS 180
DB 121 AKKRVLEPGLVEEGAKTAPGKKRPVEOSPOBDSGGIGKTGQOQPAKKRLNFGQTGDS 180
QY 181 SVDPDQPLGEPPTPAVGPPTTMASSGGA PMADNNEGADVGNASGNHCDSTWLGDRVI 240
DB 181 SVDPDQPLGEPPTPAVGPPTTMASSGGA PMADNNEGADVGNASGNHCDSTWLGDRVI 240
QY 241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHFGYSTPWGYPDFNRFFCHSPRDWQRL 300
DB 241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHFGYSTPWGYPDFNRFFCHSPRDWQRL 299
QY 301 INNNNGEPRKRLNFKLFTNIOVEKVTNDGVTIANNLSTVOYFSDSEYQLPYVLGSAHQ 360
DB 301 INNNNGEPRKRLNFKLFTNIOVEKVTNDGVTIANNLSTVOYFSDSEYQLPYVLGSAHQ 359
QY 361 GCLPPPADVFMIPQYGYLTNNGSAVGRSSFCLEYPSSQMLRTGNNFTFSYTEEVP 420
DB 361 GCLPPPADVFMIPQYGYLTNNGSAVGRSSFCLEYPSSQMLRTGNNFTFSYTEEVP 419
QY 421 FHSSTYAHQSGLRLMNP.LIDQYLYLNRTONOGSAONKDLFSRGS PAMGSAVQPNWLP 480
DB 421 FHSSTYAHQSGLRLMNP.LIDQYLYLNRTONOGSAONKDLFSRGS PAMGSAVQPNWLP 479
QY 481 GPCYRQORVSKTKTNNNSNFTTGASKYNLGRBSI INPGTAMASHKXDEDEKFFPMGCV 540
DB 481 GPCYRQORVSKTKTNNNSNFTTGASKYNLGRBSI INPGTAMASHKXDEDEKFFPMGCV 539
QY 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFGTVAVNFOSSTDPATGDVHANG 600
DB 541 MIFGKESAGASNTALDNWMTDEBEIKATNPVATERFGTVAVNFOSSTDPATGDVHANG 599
QY 601 ALPGMWQDRDYLQGPIMAKI.PHTDGHFHPSPLMGFGGLKNPPOILLKNTFVPANPRA 660
DB 601 ALPGMWQDRDYLQGPIMAKI.PHTDGHFHPSPLMGFGGLKNPPOILLKNTFVPANPRA 659
QY 661 EFSATKFAFTIOYSTGOVSVEIEMELQKENSXKRNPEVOYTSNYAKSANVDTVDNGL 720
DB 661 EFSATKFAFTIOYSTGOVSVEIEMELQKENSXKRNPEVOYTSNYAKSANVDTVDNGL 719
QY 721 YTEPRPIGTRYLTRPL 736
DB 721 YTEPRPIGTRYLTRPL 735

RESULT 12
Q6JCS2_9VIRU
ID Q6JCS2_9VIRU PRELIMINARY; PRT; 737 AA.
AC Q6JCS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)


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Db 481 LBPGRQROQSVSKTLDQNNNSNPAMTGATKTHLNGRLNLVPGVAMATHKDDEERFFPS 540
Qy 539 GWMIFGKESAGASNTALDNVMTTDEBEIKATNPVATERFGVAVNFQSSSTDPATGDVHA 598
Db 541 GVLIFGKTGA-ANKTTLENVLMNTNEBEIRPTNPVATEEYGTAVSNLQANATAAQOVVNN 599
Qy 599 MGLAQGMWQDDVYLOGPIMAKIPHTDGHFHPSPMLMGFGFLKNPPQILIKNTVPANP 658
Db 600 QALPGWVQNRDYYLQGPIMAKIPHTDGNFHPSPMLMGFGFLKNPPQILIKNTVPANP 659
Qy 659 PAEFSATKFASTFOYSTGQSVSEIEMELQKENSKRNNPEVOYTSNYAKANVDFTVDN 718
Db 660 PEVFPFAKFASTFOYSTGQSVSEIEMELQKENSKRNNPEIQYTSNFKQGTVDPAVDSQ 719
Qy 719 GLYTEPRPIGTRYLTRPL 736
Db 720 GYSEPRPIGTRYLTRNL 737

RESULT 14
Q6JC28_9VIRU PRELIMINARY; PRT; 735 AA.
ID 06JC28_9VIRU
AC 06JC28_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Capsid protein Vp1.
GN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Pubmed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530591; AAS99276.1; -; Genomic_DNA.
DR SMR; Q6JC28; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81897 MW; 197066F8911FAE9B CRC64;

Query Match 86.6%; Score 3453.5; DB 2; Length 735;
Best Local Similarity 84.5%; Pred. No. 5,5e-215;
Matches 622; Conservative 48; Mismatches 65; Indels 1; Gaps 1;

Qy 1 MADDGYLPWMLBNDNLSEGIKREWMWDLKPGAPKPKANQOKDDRGVLPGYKYLGPFGND 60
Db 1 MADDGYLPWMLBNDNLSEGIKREWMWDLKPGAPKPKAEHKGSGVLPGYKYLGPFGND 60
Qy 61 KGEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSPFGNLGAAYVQ 120
Db 61 KGEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSPFGNLGAAYVQ 120
Qy 121 AKKRVLEPIGLVEEGAKTAPGKKRPVQSPQEPDSSSGIGTKTQOPAKKRLNFGQTGDS 180
Db 121 AKKRVLEPIGLVEEVPYTAAGKKRPVHSPAEPSDSSGIGTKAKQOPAKKRLNFGQTGDD 180
Qy 181 SVDDPQPIGPRPAPVAVPTMASGGGAPMADNNEGADGVNASGNMHCDSTWLGDRVI 240
Db 181 SVDDPQPIGPRPAPVAVPTMASGGGAPMADNNEGADGVNASGNMHCDSTWLGDRVI 240
Qy 241 TTSTRTWALPTYNHLYKQISSASTGASNDNHFGYSTPWGYPDFNRFHCFSPRDMQRL 300
Db 241 TTSTRTWALPTYNHLYKQISSQSGASNDNHFGYSTPWGYPDFNRFHCFSPRDMQRL 299
Qy 301 INNNWGRPRKLNFLNIOYKEVTTNDGTTTIANNLTSVQVPSSEYQLPVYLGSAHQ 360
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Db 300 INNNWGRPRKLNFLNIOYKEVTTNDGTTTIANNLTSVQVFTDSEYQLPVYLGSAHQ 359
Qy 361 GCLPFPADVPMIPQYGLTTLNNGSQAVGRSSFYCLEFPBQMLRTGNNTFFSYFEEDVP 420
Db 360 GCLPFPADVPMIPQYGLTTLNNGSQAVGRSPFYCLEFPBQMLRTGNNTFFSYFEEDVP 419
Qy 421 FHSYAHSQSLDRLNNPILIDYLYLNRTONQSGSAQKDLFFSRGSPAGMSVQPKMLP 480
Db 420 FHSYAHSQSLDRLNNPILIDYLYLNRKTQNSGTLQOSRLFFSQAQFTNMSLOAKMLP 479
Qy 481 GPCYQQRVSKTKTDNNNSNFTMGASXYNLNGRESINPGTAMASHKDEBDFPMSGV 540
Db 480 GPCYQQRVSKTKTDNNNSNFTMGATKYHLNGRSLVNPGRAMASHKDEBDFPMSGV 539
Qy 541 MIFGKESAGASNTALDNVMTTDEBEIKATNPVATERFGVAVNFQSSSTDPATGDVHAMG 600
Db 540 LIFGKGTNANDADLENVMTTDEBEIRPTNPVATEEQYGVTSNNLQNSNTPGTGTVNNHG 599
Qy 601 ALPGWVQDDRVYLOGPIMAKIPHTDGHFHPSPMLMGFGFLKNPPQILIKNTVPANPA 660
Db 600 ALPGWVQDDRVYLOGPIMAKIPHTDGHFHPSPMLMGFGFLKNPPQILIKNTVPANPPT 659
Qy 661 EFSATKFASTFOYSTGQSVSEIEMELQKENSKRNNPEVOYTSNYAKANVDFTVDNGL 720
Db 660 NFSSAKFASTFOYSTGQSVSEIEMELQKENSKRNNPEIQYTSNFKSNNVDFTVDNNGV 719
Qy 721 YTEPRPIGTRYLTRPL 736
Db 720 YSEPRPIGTRYLTRNL 735

RESULT 15
Q6JC19_9VIRU PRELIMINARY; PRT; 738 AA.
ID 06JC19_9VIRU
AC 06JC19_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Capsid protein Vp1.
GN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Pubmed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530600; AAS99285.1; -; Genomic_DNA.
DR SMR; Q6JC19; 218-738.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 738 AA; 81582 MW; 585F46CF0769934F CRC64;

Query Match 86.6%; Score 3453; DB 2; Length 738;
Best Local Similarity 85.0%; Pred. No. 5,9e-215;
Matches 627; Conservative 48; Mismatches 61; Indels 2; Gaps 2;

Qy 1 MADDGYLPWMLBNDNLSEGIKREWMWDLKPGAPKPKANQOKDDRGVLPGYKYLGPFGND 60
Db 1 MADDGYLPWMLBNDNLSEGIKREWMWDLKPGAPKPKANQOKDDRGVLPGYKYLGPFGND 60
Qy 61 KGEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSPFGNLGAAYVQ 120
Db 61 KGEPVNAADAALAEHDKAYDQOLKAGDNPYLRYNHADAFOERLQEDTSPFGNLGAAYVQ 120
Qy 121 AKKRVLEPIGLVEEGAKTAPGKKRPVQSPQEPDSSSGIGTKTQOPAKKRLNFGQTGDS 179
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Db      121 AKRVLBEPLGLVEBAKTA PGKKRPVEBPS PORS PDSSTGIGKGOQPAKKRLNFGQTGDS 180
QY      180 ESVPPDPOPLGEPPTPAVPTTMA SGGGAPMADNNEGADGVGNASGNMHCSTWLAGDRV 239
Db      181 ESVPPDPOPLGEPPTPAVPTTMA SGGGAPMADNNEGADGVGNASGNMHCSTWLAGDRV 240
QY      240 ITTSTRTVALPTYNHLYKQISSASTGAS -NDNHFGYSTPWGYPDFNRFCHFSPRDMQ 298
Db      241 ITTSTRTVALPTYNHLYKQISSASTGAS -NDNHFGYSTPWGYPDFNRFCHFSPRDMQ 300
QY      299 RLNNNGRRPRRLNFKLFNIQVKEVTINDGYTTIANNLSTVOYFSDSEYQLPYVLGSA 358
Db      301 RLNNNGRRPRRLNFKLFNIQVKEVTINDGYTTIANNLSTVOYFSDSEYQLPYVLGSA 360
QY      359 HOGCLPRFPADVFMIPQGYLTLNNGSOAVGRSSFYCLEYFPSPOMLRTGNNPFTSPTFE 418
Db      361 HOGCLPRFPADVFMIPQGYLTLNNGSOAVGRSSFYCLEYFPSPOMLRTGNNPFTSPTFE 420
QY      419 VPFHSSYAHSGSLDRLMNPFLIDQYLYLNRTONOGSAQNKDLFSGSPAGMSVOPKXW 478
Db      421 VPFHSSYAHSGSLDRLMNPFLIDQYLYLNRTONOGSAQNKDLFSGSPAGMSVOPKXW 480
QY      479 LFGPCYRQORVSKTIDNNNSNFTWTGASKYNLNGREBIIINPGTAMASHKDEDEKFFPM 538
Db      481 LFGPCYRQORVSKTIDNNNSNFTWTGASKYNLNGREBIIINPGTAMASHKDEDEKFFPM 540
QY      539 GVMIFGKESAGASNTALDNVMTTDEBEIKATNPVATERPGTAVANFQSSSTDPAQDVHA 598
Db      541 GVMIFGKESAGASNTALDNVMTTDEBEIKATNPVATERPGTAVANFQSSSTDPAQDVHA 600
QY      599 MGALFGMWQDRDVLQGPIMAKIPHDTGHHFSPPLMGFGGLKNPPOLLKNTVPANP 658
Db      601 MGALFGMWQDRDVLQGPIMAKIPHDTGHHFSPPLMGFGGLKNPPOLLKNTVPANP 660
QY      659 PAEFSATKFASTITQYSTGVSEIEMELQKENSKRMPDEVQYTSNAXASAVDFTVDNN 718
Db      661 PTFPSQAKLASFTITQYSTGVSEIEMELQKENSKRMPDEVQYTSNAXASAVDFTVDNN 720
QY      719 GLYTEPRPIGTRYLTRPL 736
Db      721 GTYSEBRPIGTRYLTRNL 738

```

Search completed: November 23, 2005, 17:41:16
 Job time : 144.766 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2005, 17:29:19 ; Search time 25.9904 Seconds
(without alignments)
2724.684 Million cell updates/sec

Title: US-10-696-282-13

Sequence: 1 MAADGYLPDWMEDNLSEGR.....NNGLYTEPRPIGTRVLRPL 736

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2177.5	54.6	504	1 VCPV3A	coat protein - ade
2	2168.5	54.4	732	2 S52210	coat protein VP1 -
3	798.5	20.0	673	1 VCPV3B	coat protein VP1 -
4	600.5	15.1	781	1 VCPV19	coat protein VP1 -
5	482	12.1	729	1 A60006	coat protein VP1 -
6	482	12.1	729	1 VCPVNA	coat protein VP1 -
7	444.5	11.0	727	1 VCPV1F	coat protein VP1 -
8	439.5	10.8	727	1 VCPV1E	coat protein VP1 -
9	431.5	10.7	727	1 VCPV1P	coat protein VP1 -
10	426	10.6	718	1 VCPV1M	coat protein VP1 -
11	424.5	10.6	718	1 VCPV1P	coat protein VP1 -
12	421.5	10.6	748	1 VCPVCP	coat protein VP1 -
13	407.5	10.2	737	1 VCPVCD	coat protein VP1 -
14	404	10.1	722	1 VCPV12	coat protein VP1 -
15	385.5	9.7	722	1 VCPV1N	coat protein VP1 -
16	377	9.5	716	1 VCPV2M	coat protein VP1 -
17	234	5.9	587	1 B44276	coat protein VP1 -
18	199.5	5.0	810	2 A44054	orf1 protein - Jun
19	198	5.0	584	2 S49594	capsid protein VP2
20	191	4.8	702	1 VCPVAP	coat protein VP1 -
21	143.5	3.6	682	2 S50856	whn protein - rat
22	139	3.5	931	2 T49710	related to glucan
23	131.5	3.3	1446	1 A45344	immediate-early pr
24	130.5	3.3	1145	2 T18235	transcription acti
25	130	3.3	1338	2 T30565	MAP kinase kinase
26	129	3.2	1072	2 A86827	hypothetical prote
27	124.5	3.1	2493	2 A55481	adenylate cyclase
28	124	3.1	1296	2 C82521	hemolysin-type cal
29	124	3.1	3078	2 T28432	variant-specific s

30	123.5	3.1	690	2 A80124	probable TonB-depe
31	123.5	3.1	2529	2 B64635	toxin-like outer m
32	123	3.1	1142	2 T37435	enamelin precursor
33	122.5	3.1	880	1 SYBSVS	valine-tRNA ligase
34	121	3.0	635	2 P9660	protein F2K11.10 [
35	121	3.0	1113	2 S28925	nuclear pore compl
36	121	3.0	1549	2 T48103	type VII collagen
37	120	3.0	1379	2 T37752	hypothetical serin
38	119.5	3.0	1180	2 B86719	hypothetical prote
39	119.5	3.0	1394	2 S60762	IgA-specific serin
40	119.5	3.0	2004	2 AC0314	probable membrane
41	119	3.0	667	2 A41311	transcription fact
42	118.5	3.0	2399	2 H71879	toxin-like outer m
43	118	3.0	739	2 T52289	probable transkeo
44	118	3.0	956	2 T08144	myrosinase-binding
45	117.5	2.9	1076	1 A35622	nuclear pore prote

ALIGNMENTS

RESULT 1
VCPV3A
coat protein - adeno-associated virus type 2

C:Species: adeno-associated virus type 2
C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
C:Accession: A03698
R:Srivastava, A.; Lusby, E.W.; Berns, K.I.
J. Virol. 45, 555-564, 1983

A:Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome.
A:Reference number: A03694; MUID:83164299; PMID:6300419

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-504 <SRI>

A:Cross-references: UNIPROT:P03135; UNIPARC:UPI0000127C9E; EMBL:J01901; NID:9209616; PI

C:Superfamily: adeno-associated virus coat protein

C:Keywords: coat protein

Query Match 54.6%; Score 2177.5; DB 1; Length 504;
Best Local Similarity 82.5%; Pred. No. 3.9e-134;
Matches 392; Conservative 33; Mismatches 47; Indels 3; Gaps 2;

QY	203	MASGGAPMADNNEGADGVGNAGNWHCDSTWLGDRVITTTSTRMALPTYNHLYQIIS	262
DB	1	MATGSGAPMADNNEGADGVGNAGNWHCDSTWLGDRVITTTSTRMALPTYNHLYQIIS	60
QY	263	ASTGASNDNHYFGYSTPMKGYFDENRPHCHESPRDQRLINNNMGPRKLNFLNIQYK	322
DB	61	QS-GASNDNHYFGYSTPMKGYFDENRPHCHESPRDQRLINNNMGPRKLNFLNIQYK	119
QY	323	EYTTNDGVTTIANNLSTVQVFSDESYQLPYVLGSAHQCLPPFADVEMIDQYGLTLN	382
DB	120	EYTTNDGVTTIANNLSTVQVFTDSEYQLPYVLGSAHQCLPPFADVEMIDQYGLTLN	179
QY	383	NSGQAVGRSSFYCLEYFSPQMLRTGNNFTFSYTFEEVPHSSYASQSIDRLNPLIDQY	442
DB	180	NSGQAVGRSSFYCLEYFSPQMLRTGNNFTFSYTFEEVPHSSYASQSIDRLNPLIDQY	239
QY	443	LYLTARTQNSGSAQKDLIFSRGSPAGMSVQPKNMLPPCYRQGVSTKTDNNNSNFT	502
DB	240	LYLTARTQNSGSAQKDLIFSRGSPAGMSVQPKNMLPPCYRQGVSTKTDNNNSNFT	299
QY	503	MTGASKYNTNGRESIIPGTAMASHKDDDEKFPMSGWI PCKESAGASNTALDNVMTD	562
DB	300	MTGATKYHNGRDSLVNP--AMASHKDDDEKFPMSGWI IFGQSEKTNVNI EKVMITD	357
QY	563	EEBIKATNPVATERFETVAVNFQSSSTDPAATGVHAMGALPGKMWODRVIYLOGPIWAKI	622
DB	358	EEBIKATNPVATERFETVAVNFQSSSTDPAATGVHAMGALPGKMWODRVIYLOGPIWAKI	417
QY	623	PHTDGHFHSPLMGFGFLKNPPQQLIKNTPVANPAPFSAATKFSFTQYSTG	677

Db 418 PHTDGHFHPSLMGFGGLKHPPOILLIKNTVPANPSTTFSAKPFITQYSTG 412

RESULT 2

552210
coat protein VP1 - muscovy duck parvovirus
N:Alternate names: VP1 protein
C:Species: muscovy duck parvovirus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S52210
R:Zadori, Z.; Erdel, J.; Nagy, J.; Kisari, J.
submitted to the EMBL Data Library, September 1993
A:Reference number: S52209
A:Accession: S52210
A:Molecule type: DNA
A:Residues: 1-732 <ZAD>
A:Cross-references: UNIPROT:O83289; UNIPARC:UPI00000F6C5D; EMBL:X75093; NID:g609091; PID
A:Experimental source: strain FM
C:Genetics:
A:Gene: VP1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 54.4%; Score 2168.5; DB 2; Length 732;
Best Local Similarity 55.2%; Pred. No. 2.6e-133;
Matches 418; Conservative 90; Mismatches 186; Indels 63; Gaps 13;

9 DWLENDLSEGRWMDLKGAPKPYANOQK-----DGRGLVPGYKYLGFN 57
Db 10 DWYE-----TAASWHLKAGAPKPSNOOSVSTRKPKRKNNRGFVLPGYKYVGPON 65

58 GLDKSEPVNAADALEHDKAYDQOLKAGDNPLYLNHADAEPORLEDTSPGNGLRA 117
Db 66 GLDKSEPVNAADALEHDKAYDQOLKAGDNPLYLNHADAEPORLEDTSPGNGLRA 125

118 VFQAKRVLLEPLGLVEBGAKTAPGKKRPVEQSPOEPDSSSGIGKTGOOPAKKRLNFGQT 177
Db 126 VFQAKRVLLEPLGLVEBGAKTAPGKKRPVEQSPOEPDSSSGIGKTGOOPAKKRLNFGQT 170

178 DSEVDPDPOPLG-----EPATPAVAGPTTMASSGGAPADANNEGADGVGNASG 226
Db 171 --ENSPSPNSGSEASAAATBGSBPAAP-----NMAEGSGAGMDSAGADGVGNASG 222

227 NMHCSTYLGDREVITTSRTMALPTYNHLYKQISSASGASNDNHGYGSPMKYPRPN 286
Db 223 NMHCSTYLGDREVITTSRTMALPTYNHLYKQISSASGASNDNHGYGSPMKYPRPN 281

287 RFHCHFSRDMQRLINNMGFRPKRLNFKLFIQVKEVTTNDGVTTLANNLTSTQVPSD 346
Db 282 RFHCHFSRDMQRLINNMGFRPKRLNFKLFIQVKEVTTNDGVTTLANNLTSTQVPSD 341

347 SEYQLPYVLGSAHQCLPPPADVMIPOYGYLTIN--NSQAVGRSSFYCLAYPSPQM 403
Db 342 SEYQLPYVLGSAHQCLPPPADVMIPOYGYLTIN--NSQAVGRSSFYCLAYPSPQM 401

402 LRTGNFTFSTYFEEVPRFHSYAHSOSLDRLNPLIDQVLYLNTQNSGSAQKDLIF 463
Db 402 LRTGNFTFSTYFEEVPRFHSYAHSOSLDRLNPLIDQVLYLNTQNSGSAQKDLIF 455

464 SRGSPAGMSVQPKNMLPGPCYRQORVSKTK--TDNNNSNFTWTGASKYVLNGBISLNG 521
Db 466 SRGSPAGMSVQPKNMLPGPCYRQORVSKTK--TDNNNSNFTWTGASKYVLNGBISLNG 515

522 TAMASHKODEDKFPFMSGVMIFGKE--SAGASNTALDNVMTDEBEIKATNPVATERFGT 579
Db 522 TAMASHKODEDKFPFMSGVMIFGKE--SAGASNTALDNVMTDEBEIKATNPVATERFGT 575

580 VAVNQSSTDPATGIVHAMGALPGMWVDDRVYLQGPIMAKIPHTDGHFHPSLMGCG 639
Db 580 VAVNQSSTDPATGIVHAMGALPGMWVDDRVYLQGPIMAKIPHTDGHFHPSLMGCG 635

640 LKNPPOILLIKNTVPANPSTTFSAKPFITQYSTG 699

Db 636 LHNPPQVFIKNTVPADPPLLEVYNOKMNSYITQYSTGQCTVEMWELKENSKRMPBEI 695

QY 700 QYTSNPAKSAVNDVTVDNNGLYTSPRIQTRYLRLPL 736

Db 696 QYTSNPAKSAVNDVTVDNNGLYTSPRIQTRYLRLPL 732

RESULT 3

VCPVBS
coat protein VP1 - bovine parvovirus
N:Contains: coat protein VP2
C:Species: bovine parvovirus
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A26104
R:Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.; Bates, R.C.
J. Virol. 60, 1085-1097, 1986
A>Title: Complete nucleotide sequence and genome organization of bovine parvovirus.
A:Reference number: A26104; MUID:87061184; PMID:3783814
A:Accession: A26104
A:Molecule type: DNA
A:Residues: 1-673 <CHB>
A:Cross-references: UNIPROT:P07297; UNIPARC:UPI0000127D77; EMBL:M14363; NID:g333454; PID
A:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:138-673/Product: coat protein VP2 #status predicted <VP2>

Query Match 20.0%; Score 798.5; DB 1; Length 673;
Best Local Similarity 28.6%; Pred. No. 3.7e-44;
Matches 214; Conservative 105; Mismatches 275; Indels 155; Gaps 21;

30 PKPYANOQKODDGLVLPGYKYLGFNGLDKSEPVNAADALEHDKAYDQOLKAGDN 89
Db 3 PTNANKSK-----GLTPGYNYLGPFRNSLFAAGAPVNAADAAARKHDEGYDGLKEGKNP 57

90 YLRYNHADAEPORLEDTSPGNGLGRAVFOAKKRVLEPLGLVEBGAKTAPGKKRPVEQS 149
Db 58 YLRYNHADAEPORLEDTSPGNGLGRAVFOAKKRVLEPLGLVEBGAKTAPGKKRPVEQS 111

150 POEPDSSSGIGKTGOOPAKKRLNFGQTDSSVDPDPOPLGSP--PATPAAGPTTMASSG 207
Db 112 LYPARSNKGAKKAREPAPSTSNQONNEVSNIDIPDEAGNOPILATRSVVGSGSVGGG 171

208 GAPMADNNEGADGVGNASGNMHCSTYLGDREVITTSRTMALPTYNHLYKQISSASG 267
Db 172 -----RGSSGVGYSTGWTGTTIPSENIIVTKRQFICDLKNGHLYKS--EVLNFGD 222

268 SUNDHGYSTPMGYFDENRFHCHFSRDMQRLINNMGFRPKRLNFKLFIQVKEVTTN 327
Db 223 SUNDHGYSTPMGYFDENRFHCHFSRDMQRLINNMGFRPKRLNFKLFIQVKEVTTN 281

328 DGVTTIANN--LTSYQVPSDSEYQLPYVLGSAHQCLPPPADVMIPOYGYLTIN----- 381
Db 282 DGVTTIANN--LTSYQVPSDSEYQLPYVLGSAHQCLPPPADVMIPOYGYLTIN----- 341

382 GAMGVVYNNDLTAGMIFCDSDHRYVYQNHMPDQCMELNSIWEIPOVAYIPAPISV 435
Db 382 GAMGVVYNNDLTAGMIFCDSDHRYVYQNHMPDQCMELNSIWEIPOVAYIPAPISV 401

436 NPLIDQVLYLNTQNSGSAQKDLIFSRGSP-----AGMSVQPKNMLP 480
Db 436 NPLIDQVLYLNTQNSGSAQKDLIFSRGSP-----AGMSVQPKNMLP 470

481 GPCTRQQRVSKTKTDNNNSNFTWTGASKYVLNGBISLNGRSEIINPTMAASHDDEDKFPFMSGV 540
Db 481 GPCTRQQRVSKTKTDNNNSNFTWTGASKYVLNGBISLNGRSEIINPTMAASHDDEDKFPFMSGV 535

541 M-----IFGKE-----SAGASNTALDNVMTDEBEIKATNPVATERFGT 575
Db 541 M-----IFGKE-----SAGASNTALDNVMTDEBEIKATNPVATERFGT 575

576 RFGTVAVNQSSTDPATGIVHAMGALPGMWVDDRVYLQGPIMAKIPHTDGHFHPSLMG 635
Db 576 RFGTVAVNQSSTDPATGIVHAMGALPGMWVDDRVYLQGPIMAKIPHTDGHFHPSLMG 635

577 TTTREARFKLLTGSAGADGVKEMWMLPQNMWDSAPISRYPDIWVKVPRVNRKTLDTQD 576

Qy 636 GGFGLKPPQIILK-NTVPANPAEFSATKPSFTTOSTGCVSVIEIEMELOKENSK 693
Db 577 GSIPMSHPGPIFIKILARPVPGND-----SFLNIYVYTGQVSGEVWEVEKRGTK 627
Qy 694 RKNPEVOTSNYAKSAND-FIVDNNGLY 721
Db 628 NMRPEYMS--ATNMSVDATYINNAGVY 653

RESULT 4

vcprv19
coat protein VP1 - parvovirus B19 (strain Au)
C:Species: parvovirus B19
A:Note: host Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A24299
R:Shade, R.O., Blundell, M.C.; Cotmore, S.F.; Tattersall, P.; Astell, C.R.
J. Virol. 58, 921-936, 1986
A:Title: Nucleotide sequence and genome organization of human parvovirus B19 isolated fr
A:Reference number: A24299; MUID:86200451; PMID:3701931
A:Accession: A24299
A:Molecule type: DNA
A:Residues: 1-781 <SHA>
A:Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; EMBL:M13178; NID:G333375; PID
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 15.1%; Score 600.5; DB 1; Length 781;
Best Local Similarity 26.6%; Pred. No. 3.5e-31; Indels 107; Gaps 20;
Matches 182; Conservative 95; Mismatches 300;

Qy 47 LFGYKYLGPFGNGLDKGEPEVNAADAALHEDKAYDOOLKAGDNPYLRYNHADAEPERLOE 106
Db 125 LFGTYVVGNGELQNGPQSAVDSARINDPRYSQAKLGINPYTHMTVADELLKNIKN 184
Qy 107 DTSPGNGLGRAVFOAKKRVLEPLGLVEBAGKTAPEKKRVEGSPQEPDSSSGIGTKGQOP 166
Db 185 ETGFQAOVAKDYF-----TLKGAALPAVAFHQ-----GSLPEVP 217
Qy 167 AKKRLNFGQTGSESEVPDQPLGEPRPATPAVGPPTMAAGGAPMADNNEGADVGNAG 226
Db 218 ATNA-----SEKYPMSITSVASASTGA-----GGG-----GSNSVKS 250
Qy 227 NNHCSTWLGDRIYTTSTRTMALPTYNNHLYKOISASTGASND-----NHIFY 276
Db 251 MMSGATPFSANVTCTFSQFLIPYRPEHHYKFSRASSCHNASKEAKVCTISPIWY 310
Qy 277 STPMGFDENRPHCHSPRDWQRLINNMGFRPKRLNFKLFNIQVEVT--TNDVTTTA 334
Db 311 STPMRYLDNALNLFPSPLEPQHLIENYGSIAFDALTITISEIAVDVDTKGQGV-QVT 369
Qy 335 NNLTSTVOVFSDEYOLPYVLGSAHGCCLPPPADVFMIPQCYLILNN-GSAYG----- 389
Db 370 DSTTGLCMLVHEHYRYPVLAGGQDTLAPELPIWYPPPOYAYLLVGVGNTVGLISGSK 429
Qy 390 -----RSSFYCLEYFSPQMLRTGNNTFTSYFEEVPHSSYAHOSGLDRLMPLIDQY 444
Db 430 KLAESASATYVLEHSHFOLLGTGCTASMKKPPVPEMLGSCQIFEMYNL---YGS 486
Qy 445 YLNRTONSGSANKDILFSRSGPAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSFTWT 504
Db 487 RLGVPRDLTGDPKFRSL-----THEDHAIOPQNFMGPLVNSVSTEGDSSTNGAKALT 541
Qy 505 GASKYLNREGSLING-TAMASHKDEDEKFFPMGVMIFGKESAGASNTALDNV----- 558
Db 542 GLSTGTSQNTSLRGPVVSQPYHMDTKYTGAINAISHGQTTYG---NAEDKEXYQGY 598
Qy 559 --MITDEBEIKATNPATERFGTAVANFOSSSTDPATGVDHAGALPGMWQODRDVYLQ 616
Db 599 GRPNKEQOLKOLGIMHTY-----FRPKGQOYTDQLE-RPLWVGSVNNRRLHYES 651
Qy 617 PIWAKIPHTDGHFHS-PLMGSGFLKNPPQIILKNTVPANPAEFSATKPSFTTOST 675

Db 652 QLMKRIPLDLSFRTQFALAGKGLHQPPPIFLK--ILPQSGPIGKISMGITTLVGYA 709
Qy 676 TGQVSVIEIEMEL-QKENSRRNPE 698
Db 710 VGIMTVTWTFTKLGPRKATGTRWNPQ 733

RESULT 5

A60006
coat protein VP1 - porcine parvovirus (strain 90HS)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A60006
R:Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
A:Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A:Reference number: A60006; MUID:89319168; PMID:2750278
A:Accession: A60006
A:Molecule type: DNA
A:Residues: 1-729 <SAR>
A:Cross-references: UNIPROT:P33484; UNIPARC:UPI0000127C6E
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; glycoprotein
F:151-723/Product: coat protein VP2 #status predicted <VP2>
F:172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #statd

Query Match 12.1%; Score 482; DB 1; Length 729;
Best Local Similarity 25.7%; Pred. No. 1.7e-23;
Matches 197; Conservative 112; Mismatches 314; Indels 144; Gaps 35;

Qy 43 RGLVLPYKYLGPFGNGLDKGEPEVNAADAALHEDKAYDOOLKAGDNPYLRYNHADAEPER 102
Db 9 RGLTLPGYKYLGPFGNSLDGSEPTNPSDAAKEHDEAYDKYISGKNPFYFSADEKFTK 68
Qy 103 RLQEDTSGNULGRAVFOAKKRVLEPLGLVEBAGTAPGKKRVEGSPQEPDSSSGIGK- 161
Db 69 ETEHAKDTGKGIKGYFFRA-KAARF--KLSTDSPTTSQDEVRSPKMGSKRPPGR 125
Qy 162 -----TGQAPAKKRLNFGQTGSESEVPDQPLGEPRPATPAVGPPTMAAGGAPMA 212
Db 126 PAPRIHIFNLAKKRAKSGNTSNMSMSNVBEHNNINNGTEL-SATNGNSGGGGGGG--- 181
Qy 213 DNNEGADVGNASGMW--CSTWLGD--RVITSTRTMALPTYNNHLYKOIS--SAST 265
Db 182 -GGRGAGGVGVTGSPFNQTEFOYLGEGLVRTAHASRLIHLMPEHEHYKRIHYLNSBS 240
Qy 266 GAS-----NDNHFGYSTPMGYDFPRPHCHSPRDWQRLINNMGFRPKRLNFKLFNIQV 321
Db 241 GVAAGMVDADATQMTWTPMSLIDANAGVGFEPADWOLISNMTEINLVSPQEBIFNVVL 300
Qy 322 KEVT--TNDVTTIANLSTVOVFSDEYOLPYVLGSAHGCCLPPPADVFMIPQCYL 378
Db 301 KTTTSATSPPKIKIYNNDLTASIMVALDTNNLTPTTPAARSETLGFYWLPTKPYQYX 360
Qy 379 L-----TLNNGSAQVRS-----SFYCLE-YFSPQMLRTGNMF-TSYTYE 417
Db 361 YLSTCRNLNPPYTGOSQOITDSIQGLSHDIMFYTIENAVDIIHLRTGDEPSTGIYHD 420
Qy 418 EYFPHSSYAHOSGLR-----LMNPLI--DOYLYLNRTONSGSANKDILFSRSG 467
Db 421 TKPL--KLTHSQTRSLGLPKLLTEPTBGDQHEGTLPPAANTRGHTQTMNSTYET 478
Qy 468 PAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSFTWTGASKYLNREGSLINP--GTAMA 525
Db 479 ----AIRP-----AQGVNPPYNNFYSNCGP-----LTPVPTADT 512
Qy 526 SHKDEDEKFFPMGVMIFGKESAGASNTALDNVMTDEBEIKATNP-----VATERFGT 579
Db 513 QVNDDE-----PAGAIRFTWGYOHGQLTTS-----SOELERYTFNPOSKCGAPRKOQFO 562
Qy 580 VA-VNFOSS-----TDPATG--DVHANAGALP-----GMWQODRDVYLQGPIMAKI PHT 625

```
Db 563 QAPLNLENTNNGTLLPSPDPIGCKPMHFMNTLNTYGPULTALNNTAPVPNGQIWDKELDT 622
Oy 626 D--GHFHSPLMGCGFLK-NPPQILIKNTVPANPAPFSA-TKFASTIQTGYSTGV 681
Db 623 DLKPRLLH--VTAPFVCKNNPPGOLFVKIAP---NLTDFFNADSPQOPRIITYSNFWMG 676
Oy 682 EIEWELQENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIG 728
Db 677 TLTFAKKRSSNMNPIQOHTT-----TAENIGNYI-PTNIG 712

RESULT 6
VCPVNA
coat protein VP1 - porcine parvovirus (strain NMDL-2)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: B33743; D48472
R:Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compan, R.W.
Virology 173, 368-377, 1989
A>Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal pa
A:Reference number: A33743; MUID:90085785; PMID:2596019
A:Accession: B33743
A:Molecule type: DNA
A:Residues: 1-729 <VAS>
A:Cross-references: UNIPROT:P18546; UNIPARC:UPI0000127C70; GB:M32787; NID:g332983; PIDN:
R:Begeer, J.; Menezes, J.; Tjissen, P.
Virology 197, 86-98, 1993
A>Title: Genomic organization and mapping of transcription and translation products of t
A:Reference number: A48472; MUID:94025614; PMID:8212598
A:Accession: D48472
A:Molecule type: DNA
A:Residues: 11-729 <BER>
A:Cross-references: UNIPARC:UPI0000174965
A:Experimental source: NMDL-2, ATCC VR-742
A:Notes: sequence extracted from NCBI backbone (NCBI:138789, NCBI:P138794)
C:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein, glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 12.1%; Score 482; DB 1; Length 729;
Best local similarity 25.5%; Pred. No. 1.7e-23;
Matches 197; Conservative 111; Mismatches 310; Indels 154; Gaps 35;

Oy 43 RGLVPGYKYLGPFGNLDKGEFVNADAALHDKAYDQOLKAGDNPYLRYNHADAFOE 102
Db 9 RGLTLPGYKYLGPFGNSLDGSEPTNSDAAKEDHDAIKYIKGNPFFYPSADKERTIK 68
Oy 103 RLQEDTSPGNLGRAVFOAKKRVLEPLGLVEGAKTAPGKKRPVQSPQEBDSSSGICK- 161
Db 69 ETEHAKDVGKIGHFYFPAKRAFAPKL---SETDSPTTSQOPVARRSPKPHGSKRPGR 125
Oy 162 -----TSGQAPKKLNFQGTGDSVPDPOGLGEPAPRAVAGPTTASGGGAGMA 212
Db 126 PAPRHIFINLAKKKAKGTSNTNSMSSEVQHNINAGTEL-SATYGESGGGGG--- 181
Oy 213 DNNEADGVGNASG--NMHCSTWLGDD--RVITSTRTWALPTYNHLYKOIS--SAST 265
Db 182 -GGRAGGVGVTGFNNOTEFQYLGELVRLTAASRLIHLMMEBHETRYKRIHYNBS 240
Oy 266 GAS---NDNHFGYSTPWGDFNRFCHFSPRDMORLINNMWFRPRRLFKLFNIQV 321
Db 241 GVAQGVQDDAHTQMTFMSLIDANAWGVFNPADWQLISNMTEINIVSFOEIFNVIL 300
Oy 322 KEVT---TNDGVTIANNTLSTVOVFSDBEYOLPYVLSAHGCGCPPPADVFMIPQYX 378
Db 301 KTTTSATSPPTKIIYNNDLTASLMVALDTNNTLPTTAPAPRSETTGFPWMLPTKQYRY 360
Oy 379 L-----TLNNGSAVGRS-----SFYCLE-YFPGMLRTGNPF-TFSYTFE 417
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Db 361 YLSCTRNLNPPYTGQSQQTDSIQTGHSIDIMEYTIENAVPIHLTLTGDEFSGIYHFD 420
Oy 418 EVPHSSYASQSLDR-----LNMPLI--POYLYLNRRTQNSGAGNKDLFSGS 467
Db 421 TKPL--KLTHSWQTRSLGLRPKLLTEPTGDDHPTCLPAANTKRYHOTINNSYTEAT 478
Oy 468 PAGSVQPKMWLPGPCYRQORVSKTKTDNNNSNETWTGASKYNLNGRESIINP--GTMA 525
Db 479 ----AIRP-----AQVGYNTPYNNEVNGGPF-----LTPVLPADT 512
Oy 526 SHKDDKDFPPMGWMIFGESAGASNTALD--NVMITDEBEIK--ATNP-----VAT 574
Db 513 QYNDEBN-----GAIRFTMDYGHGLTTSQELERTYTFPOSCKGRAPK 557
Oy 575 ERFGTVA-VNPOSS-----TDPANG--DVHAMGALP-----GMVQDDVYLCQPIWA 620
Db 558 QQFNOQAPLNEINTNGLTLPSPDIGKSNMHEFNTLNTYGPULTALNNTAPVPNGQIWD 617
Oy 621 KIPTHD--GHFHSPLMGCGFLK-NPPQILIKNTVPANPAPFSA-TKFASTIQTGYST 676
Db 618 KELDTDLKPRLLH--VTAPFVCKNNPPGOLFVKIAP---NLTDFFNADSPQOPRIITYSN 671
Oy 677 GQVSVIEIEWELQENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIG 728
Db 672 FWMKGTLLTFAKKRSSNMNPIQOHTT-----TAENIGNYI-PTNIG 712
```

RESULT 7

VCPVIF

coat protein VP1 - feline panleukopenia virus

N:Contains: coat protein VP2

C:Species: feline panleukopenia virus, FPLV

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: A03701

R:Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winsten, S.; Hahn, W.

J. Virology 55, 574-587, 1985

A>Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv-

A:Reference number: A03697; MUID:85265017; PMID:2991581

A:Accession: A03701

A:Molecule type: DNA

A:Residues: 1-727 <CAR>

A:Cross-references: UNIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:g333474; PID:

C:Genetics:

A:Introns: 11/1

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein

F:144-727/Product: coat protein VP2 #status predicted <VP2>

F:14-727/Product: coat protein VP2 #status predicted <VP2>

```
Query Match 11.1%; Score 444.5; DB 1; Length 727;
Best local similarity 23.7%; Pred. No. 4.6e-21;
Matches 187; Conservative 117; Mismatches 255; Indels 189; Gaps 35;

Oy 43 RGLVPGYKYLGPFGNLDKGEFVNADAALHDKAYDQOLKAGDNPYLRYNHADAFOE 102
Db 10 RGLVPGYKYLGPFGNSLDGSEPTNSDAAKEDHDAALYLRSGKNPFLYPSADKERTIK 69
Oy 103 RLQEDTSPGNLGRAVFOAKKRVLEPLGLVEGAKTAPGKKRPVQSPQEBDSSSGICKT 162
Db 70 QTKDALTQWGGKIGHYFPAKKAIAVLDTDPHSTSPRTK-PTKRSKPRHIFINLAK- 127
Oy 163 GQOPAKKRLNIGQGDSESVP---DPOPLGEPPA--TPAAVGPPTTASGGGAGMAADNE 216
Db 128 -----KKKAGAGQYKRDNQAPMSGAVQPDGQGAIVNERRATGSGNSGGGG-----CG 176
Oy 217 GADGVGNASGNM-----CDSTWLGDRVITSTRTWALPTYNHLYKOI-----SS 262
Db 177 GSGGVGISTGFENNQTEFKFLENGCV--ETPANSRLVHLNMPSESEYKRVVANNMDKTA 234
Oy 263 ASTGASNDNHFGYSTPWGDFNRFCHFSPRDMORLINNMWFRPRRLFKLFNIQYX 322
Db 235 VKGNMALDDTHVQVITPMSLVADANAWGVFNPADWQLIVNTMSBLHLVFSFOEIFNVVLK 294
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Db      70 QTKADKMGKIGHYFFRAKKAIAFLVTDTPDHPSTSRPTK-PTKRSKPPHPIFINLAK- 127
Qy      163 GQAPKAKRLNGQOTDSESV-----DPOLEGPPA--TPAVGPTTMAAGGAPMADNNE 216
Db      128 -----KKKAGAGQVRNDLAPMSDGAVDPDGGQPAVRNERATGSGNGSGGG-----GG 176
Qy      217 GADVGNAAGMWH-----CDSTWLGDRVITTTSTRTWALPTYNHLYKQI-----SS 262
Db      177 GSGGIGISTGTFTNNQTEPFLENGWV--EITANSRLVHLNMPSEBENKRVVYNNMDXTA 234
Qy      263 ASTGASNDNHFGYSTPMGYFDNFRFHCFSPRDMQRLINNMGPRPKLNFKLFNIOVK 322
Db      235 VKGNALDLDIHQIYITPMSLYDANAMGWFFNPGMQLIVNTMSSELHVSFEQELINVLK 294
Qy      323 EYT-----TNDGYTTIANNTLSTVQVPSDEYOLPYVLGSAHQCL-----PPFA----- 368
Db      295 TVSSSATOPRTKRVYNNDLTASLMAVLDSTNMTPEPPAAMRSETLGFYPMKPTIPIPMKY 354
Qy      369 ---DVFMIPQGYLTLNNGSAVGRS-----SFYCLE-YPPSQMLRTGNF-TFS 413
Db      355 FQWDRTLIPSH-----TGTSGTPTNVYHGTDPDVGFTYTIENSVPVHLRTGDEFATGT 408
Qy      414 YTFEEVPRPHSSYAHQSGLDRLMN--PLIDQYLYINRTONOGSAQNKDLFSGSPAGM 471
Db      409 FFFDCKP--CRLLHTWQTNRAFGLP-----PLNSLPQSRGATNFGDIGVQDQKRGV 459
Qy      472 S-----VOPKN-MLGPCYQQRVSK-----TKTDNNNSNFTWT 504
Db      460 TOMGNTDVTYTAETTKRPAVGVSAPIYSFEASTQRPFTPIAAGGCAQTDENQA---D 516
Qy      505 GASKY---NLNGRESLINPQT---AMASHKDEDEKFFPMGSMIFGKESAGASTALD- 556
Db      517 GQPRVAFRGHQKQKTTTGTETPERFYIAHQDT-----GRYPEDMTIQINIF 563
Qy      557 NMTITDEEIKATNPVATERTFGTVAVNFQSSSTDATGVDVHAMGLPKGMWODRVDYVLOG 616
Db      564 NLPVNDVNLPTDIDIG---GKTGINY--TNIPTNYGPTALINVV-----PVYRNG 610
Qy      617 PIWAKIPHTDGHFHPSLMGFGLK-----NPPQILIKMTVPAN---PPA 660
Db      611 QIWDKEPDT-----LKRRLHVNAPRYCQNNCPQQLPKVAPNLTNYYDPDA 657
Qy      661 EFSATKFASTITQVSTGVSEIEMLEKENSKRNNPEVOYTSNYAKSANVDFTVNNGL 720
Db      658 SANMR-----LYTSDFMWKGKLVKAKLRASHTNMPLQOMSI-----VDNQFN 703
Qy      721 YTEPRPIG 728
Db      704 YV-PNNIG 710

RESULT 10
VCPVPP
coat protein VP1 - porcine parvovirus
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B33302
R:Ranz, A.I.; Mancius, J.J.; Diaz-Aroca, B.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A:Title: Porcine parvovirus: DNA sequence and genome organization.
A:Reference number: A33302; MUID:90010964; PMID:2794971
A:Accession: B33302
A:Molecule type: DNA
A:Residues: 1-723 <RAN>
A:Cross-references: UNIPROT:P18546; UNIPARC:UPI0000174964; EMBL:DD0623
A:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:145-723/Product: coat protein VP2 #status predicted <VP2>
Query Match 10.7%; Score 426; DB 1; Length 723;

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Best Local Similarity 24.9%; Pred. No. 7.3e-20;
Matches 190; Conservative 109; Mismatches 308; Indels 156; Gaps 36;

Qy      53 LGPENGIDKEPVAADAALAEHDKAYDQOLKADNLYLRNHNDAFGEHLQSDTSPG 112
Db      13 LGPNSLDQGPVNPDAALAEHDEAYDKYISKNTLPYFSADEKFKETBAKDTGG 72
Qy      113 NLGRAVQAKKRVLEPGLVEGAKTAPKKRPVEQSPQESDSSGIQK-----T 162
Db      73 KIGHYFFRAKRAFAPKL---SETDSPTTSQPEVRARSRPKHPSGKPPQKRAPRAPHIFNL 129
Qy      163 GQAPKAKRLNGQOTDSESVDPDPOLEGPPATP-AAVGPTTMAAGGAPMADNNEGADV 221
Db      130 AKKAKAKSTNNSMSSENVQGNPIN--AATBELSAGNESGGGGG-----GGRGAGV 183
Qy      222 GNAAGMWH---CDSTWLD-----RVITTSRTWALPTYNHLYKQI-----SSASTGAS-ND 270
Db      184 GVSTGFSFNNQTEFOYLGSLVRYTAHASRLIHLMPHEHYKRIHVLNSBSGSAQOMYQD 243
Qy      271 NHYFGYSTPMGYFDNFRFHCFSPRDMQRLINNMGPRPKLNFKLFNIOKVEYV---TN 327
Db      244 DAHTQMTPLMSLIDANAMGWFFNPDQMLISNNMTLNIVSFEQALFNVLKTTESATS 303
Qy      328 DGVTIANNTLSTVQVPSDEYOLPYVLGSAHQCLPPFPADVPMIPOYGYL----- 379
Db      304 PPTKIYNNDLTASLMAVLDNTNLTPTPAARSETLGFYPMKPTQYRYLSCIRNLN 363
Qy      380 ---TLNNGSAVGRS-----FYCLE-YFPQMLRTGNF-TFSYTFEEVPRPHSSYA 426
Db      364 PPTYGQSQPNRNLNTRNLHSDIMFYTTENAVPIHLRTGDEFTGTYHFTKPL--KLT 421
Qy      427 HSQSLDR-----LNNPLI--DOYLYLNRTONOGSAQNKDLFSGSPAGMSVQPK 476
Db      422 HSWQTNLSLGRPKLLEPFTBQHPGTLPAANTRGYHGTINNSTYEA---AARP- 476
Qy      477 NMLGPCYQQRVSKTKTDNNNSNFTWTGASKYVNLNGRESLINP--GTAMASHKDEDEK 534
Db      477 -----AQVGNTPYNMFYSNGPF-----LTPIVPTADTQYNDDESN- 514
Qy      535 FPMGSMIFGKESAGASTALD---NMTITDEEIK--ATNP-----VATERGTVAV- 582
Db      515 -----GALRFTMDYOHGHLTSSQELERTFPPQSKGRAPKQDPRQOAPL 560
Qy      583 NFOSS-----TPRATG--DVHAMGALP-----GMWQDRVDYVLOGPIWAKIPHTD--G 627
Db      561 NLENTNNTLLPSPIGSKSMHFMNTLNTYGPRLTALNTAPVPPNGQIWKXELDIDCKP 620
Qy      628 HHPSPMLMGFGFLK-NPPQILIKMTVPANRPAFSA-TKFASTITQVSTGVSEIEM 685
Db      621 RLH---VTAPVVCCKNNPFGQLFVKIAP---NLTDFFNADSPQOPRIITYSNFMWKGTLTF 674
Qy      686 ELQKENSKRNNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIG 728
Db      675 TAKRRSSNMNMPIQOHTT-----TAENIGKTYI-PTNIG 706

RESULT 11
VCPVIM
coat protein VP1 - minute virus of mice (strain MMV1)
C:Species: minute virus of mice, murine parvovirus
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: B23008; B29510
R:Sahl, R.; McMaister, G.K.; Hart, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A:Title: DNA sequence comparison between two tissue-specific variants of the autonomous
A:Reference number: A23008; MUID:85242059; PMID:3855242
A:Accession: B23008
A:Molecule type: DNA
A:Residues: 1-718 <SAH>
A:Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; NID:g60918; PIDN
R:Abteill, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. 57, 656-669, 1986
A:Title: DNA sequence of the lymphotropic variant of minute virus of mice, MMV(1), and c

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RESULT 13

VCPVCD

coat protein VP1 - canine parvovirus (strain CPV-8)

N:Contains: coat protein VP2

C:Species: canine parvovirus, CPV

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A31163

R:Partieth, C.R.; Aguadro, C.F.; Carmichael, L.B.

Virology 166, 293-307, 1988

A:Title: Canine host range and a specific epitope map along with variant sequences in th

A:Reference number: A31163; MUID:89020796; PMID:3176341

A:Accession: A31163

A:Molecule type: DNA

A:Residues: 1-737 <PAR>

A:Cross-references: UNIPROT:P17455; UNIPARC:UPI0000127D7A; EMBL:M23255; NID:g333467; PID

C:GeneInfo:

A:Introns: 26/3

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein

F:584-737/Product: coat protein VP2 #status predicted <VP2>

Query Match 10.2%; Score 407.5; DB 1; Length 737;

Best Local Similarity 22.8%; Pred. No. 1.2e-18;

Matches 181; Conservative 112; Mismatches 301; Indels 201; Gaps 32;

42 GGGVLPGYKYLGPFGNGLDKGRPVNAADAALEHDKAYDQOLKAGDNPYLRYNHADAEFQ 101

19 GGGKDLITYKYLGPFGNSLDQGRPTNPBDAKAEHDEBAYLYRSKPNLYLFSPADQRFI 78

102 ERLQEDTSPFGNIGRAVFOAKKRVLEPLGLVEGAKTAPGKKRPVEQSPQEDSSGIGIK 161

79 DQTKAKMKGKIGHYFFRAKKAIAVLDTDPDHSPTK-PTKRSKPRHIFINLAK 137

162 TQOQAKKRLNQGQDSDSVP---DPOPLSEPPA--TPAAVGTMTASGGGAGMADNN 215

138 -----KKKAGAGQYKRDMLAPMSDQAVQPDGQDPAVNERATGSGNGSGGG-----G 185

216 EGADGVGNASGMNH-----CDSFTLGDRAVITTSRTMALPTYNHLYKQI-----S 261

186 GSGGGGISTGTFNNOTEFKFLNGV--ETIANSRLVHLMPSENYRRVYVNNMOKT 243

262 SASGTASNDNHFGYSTPWGDFDPRFCHFSPPDMQRLINNMGFRPKRLNFKLFIQV 321

244 AANGMALDIDHAIQVTPMSLYDANAMGWFMFGMQLVNTMSLHLVSFEQELFNVL 303

322 KEVT---TNDGVTTANNITSTVOYFSDSEYQLPVYLGAHQGC-----PPPA----- 368

304 KTVSSGATOPPTKYVNNDLTASLWALDSNNMPTTPAPAMRSETLGFPYMKPTIIPTRRY 363

369 ----DVFMIPQYGYLTNNGSAVGRS-----SFYCLE-YFPSSQMLRTGNF--TF 412

364 YQWMDRTLLPSH-----TGTSGTPTNIYHGTDPDDVOQYTTIENSVPVHLTLTGDFATG 417

413 SYTFEEVPRHSSVYASOSLDRLMN--PLIDQYLYLNTONOGSQAONKDLFSRGPAG 470

418 TFFPDCRP--CRLLTHWQTRALGLRP-----FLNSLPQSBGATNEDI-----G 460

471 MSVQPRKMLPGPCYRQQRVSKTKTDNNNSNF-----TWTGASKTNLNGRESIINP- 520

461 V-----QODKRGVTOGNTNYITTEATIMPAEYGSAPYYSFEASTOGPF 506

521 ----GTAMASHKDDDEKFFPMGVMIFGKESAGASNTALD----- 556

507 KTRPIAAGGAGQDDEQAADGNPRYAFGRHQOKTTTGTETPERFTYIAHODTGRYPBGD 566

557 -----NMTTDEERIKATNPATERFGTVAVNFQSSSTDPATGVDHAMGALPGWVQD 609

567 WTONINFNLPTNDNVLLPTDPIG--DKTGNTY--TWIENYGLTALNNVP----- 614

610 RUVYLQGPYIAKIPTHTGHFHSBPLMGFGLK-----NPPQILLIKTTPVPA 656

615 -RVYPMGOIWDKEFDTD-----LKRRLHVNAPFVCONNCPQLFVKAENLT 660

QY 657 N---PPAEFATKFEAFITQYSTQVSEIEWELQKNSKRWNEVOYTSNYSKANVDF 713

DB 661 NEVYDPDASAMNSR-----IVTVSDPFWMKGLVFKAKLAASHTWNIQOMSTIN----- 707

QY 714 TVDNNGLYTEBRPIG 728

DB 708 -VDNQFNIV-PSNIG 720

RESULT 14

VCPV2

coat protein VP1 - parvovirus H1

C:Species: parvovirus H1

A:Note: host Homo sapiens (man)

C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004

C:Accession: A03699

R:Rhode III, S.L.; Paradiso, P.R.

J. Virol. 45, 173-184, 1983

A:Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybr

A:Reference number: A03695; MUID:83112183; PMID:6823009

A:Accession: A03699

A:Molecule type: DNA

A:Residues: 1-722 <RHO>

C:Cross-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D; EMBL:X01457; EMBL:J02198

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein

Query Match 10.1%; Score 404; DB 1; Length 722;

Best Local Similarity 23.3%; Pred. No. 2e-18;

Matches 175; Conservative 108; Mismatches 290; Indels 178; Gaps 30;

57 NGLDKGEVNAADAALEHDKAYDQOLKAGDNPYLRYNHADAEQERLQEDTSPFGNIGR 116

12 NSLDQGEPTNSDAAAEHDEBAYDQYIKSGNPNLYLFSPADQRFIDQTKAKMKGKYGK 71

117 AVFOAKKRVLEPLGLVEGAKTAPGKKRPVEQSPQEDSSGIGIKTQO--PA----- 167

72 YFFRTKAFAPKLSTDS-----PG-----TSGVSRPKRTKPAHIFVQ 112

168 ----KRLNFGQTDSDSVPDPOPLSEPPA--TPAAVGTMTASGGGAPMADNNEGADGVN 223

113 ARAKKASLAAQQRLLTMSDGTETNPDTGIANAVERSADGGS--SGGGSGGGGIGV 171

224 ASGMNHCDSTW--LGDRAVITSTRMAL-----PYYNHLLYKQISSASTGA 267

172 STGYNDQYTKFGLDQVETITASRLHLGMPSENYCYVYHANNQTTGHGTRKYGKM 231

268 SNDNHFGYSTPWGDFDPRFCHFSPPDMQRLINNMGFRPKRLNFKLFIQVKEVTT- 326

232 AYDTHQQLW--TPMSLYDANAMGWFOPSDQFQIONSMESLNLDSLQELFVVVVKVTBQ 290

327 ----NDGVTTANNITSTVOYFSDSEYQLPVYLGAHQGC-----PPPAD--VPMI 373

291 QGAGQDAIKVYNNDLTACMVALDSNNILPTPAQTSSETLGFPYMKPTAPAPRYVFM 350

374 POYGYLTNNGSO-----AVG-----RSSFYCLE-YFPSSQMLRTGNFTE-SYTFEEV 420

351 PROLSVTSNSABGTQITDTIGBPOALNSQFTIENTLPTLLRTLTGTGDEFTTGYIFNTP 410

421 FHSSYA-----HSQSLRLMN--PLIDQYLYLNTONOGSQAONKDLF----- 463

411 LKLHTHTQNNHACLQGITDLPISDTATSLTANAGRFGSTGTQONVVYVEALRTPAQ 470

464 -----SFGSPAGMSVQPRKMLPGCYRQQRVSKTKTDNNNSNFWTGASKTNL 511

471 IGFMDPHDNFEANQSGPKVVPV-----LDITAGBDHNN-----GAIREFNY 513

512 NGR--ESTINGTA-----MASHKDDDEKFFPMGVMIFGKESAGASNTALDVM 559

514 GKQHEBMAKQGAABERTYMAIDSAAGRDTRACFV-----QSAPISTIPNOKOI 563

560 ITDEBEIKA--TNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGWVQDRTVYLOGPI 618

```

Db      564 LQREDIAGRTMHTYNNVNSYGLSAPHPDP-----ITPNGOI 603
QY      619 WAK---IPTDGHFHPSPLMGFGGLKNPPQILIKNTVPVNPAPAEF--SATKFASTIQ 673
Db      604 WKKEIDLEHKRPLHATAPFV---CKNNPFGQLFVHLGF---NLTDQFDNSTTTSRIYV- 656
QY      674 YSTGOVSVEIEMELÖKENSKRNPVEQYTSN 704
Db      657 YSTFWYKGIKFKAKLRPNLTWNPVYQATTD 687

RESULT 15
VCEPVC
coat Protein VP1 - canine parvovirus (strain 780929)
N:Contains: coat protein VP2
C:Species: canine parvovirus, CPV
C:Date: 30-Jun-1987 #sequence_rev1sion 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03702
R:Rhode III, S.L.
J. Virol. 54, 630-633, 1985
A:Title: Nucleotide sequence of the coat protein gene of canine parvovirus.
A:Reference number: A03702; NCID:85185696; PMID:3989914
A:Accession: A03702
A:Molecule type: DNA
A:Residues: 1-722 <RHO>
A:Cross-references: UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL:M10989
C:Genetic8:
A:introns: 11/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:139-722/Product: coat protein VP2 #status predicted <VP2>

Query Match          9.7%; Score 385.5; DB 1; Length 722;
Best local Similarity 22.8%; Pred. No. 3, 1e-17;
Matches 178; Conservative 118; Mismatches 297; Indels 189; Gaps 35;

QY      49 GYKYLGPFGNGLDKGEVNNADAALBHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDT 108
Db      11 GYKYLGPFGSLDQGEPTNPDAAKEHDEAYAYLRSKKNPYLYFSPADQRFIDQTKDAK 70
QY      109 SFEGNIGRAVFOAKKRVLEPLGLVEGAKTAPGKRPVEQSPQEPDSSSGIGTGQOPAK 168
Db      71 DMGKGIQHYFFRAKKAIAPLTDTDPHPSRSTSRPTK--PTKRSKRPPIHFINLAK-----K 123
QY      169 KRINPQOTGDSESP---DPOPLGEPPA--TPAAVGPTTMASSGGA-PMAUNNEGADGVG 222
Db      124 KKAAGAOVKRDNLAIPMSDGAIVPDGQOPAVRNERATGSGNGSGGG-----GGSGGAVG 177
QY      223 NASGNMH-----CDSTWLGDRVITTSRTWALPTYNNHLYKQI-----SSASTGAS 268
Db      178 ISTGTNNQTEFEKLENGWV--ETANSSRLVHLNMPESSEKDRVYVNNMDKTAVANGMA 235
QY      269 NDNHVFGYSTPWGYFDPNRFCHPSPPDQRLINNMGFRPKRLNFKLFNIOYKEVT--- 325
Db      236 LDDIHAQIVTPWSLVDANADVWFNPGDQILVITWSEHLVSPGEDEIFNVVLKTVSESA 295
QY      326 TNDGVTIANNLSTVOVFSDESQLPYVLGSAHQCL-----PPPPA-----DVF 371
Db      296 TQPPTKYNNNDLTAASLWALDSNNTMPPTPAAMRSETLIGYPMKFTIPTPRRYIFQMDRT 355
QY      372 MIPQYGLTLANGSOAVGRS-----SFYCLE-YPPSOMLRTGNF--TFSYTFEEV 419
Db      356 LIESH-----TGTSGTPTNIYHGTDDVQFYTIENSVPVHLRLRTGDEFATGTFPFDCK 409
QY      420 PFHSSVYHSGSLRLNPLIDQYLYLNTQONOS-----GSAQNK-----D 460
Db      410 P--CRLTHTWQTNBALG--LPPLINSLPOSEGATNPGDIGVPQDKKRGVYTMGNNTYITE 465
QY      461 LLEFGRSPAGMSVQ-----PKNMLGQPCYRQGRVSKTKTDNNNSNFTWTGASKY- 509
Db      466 ATIMRPAEVSADYVFEASTOGPFKTLPIAAGR---GGAQTDENQA-----ADGNRYA 517
```

```

QY      510 -NLNGRESINPGT-----AMASHKDDKDEKFFPMGSGVMI FGKESAGASNTALD--NVMITD 562
Db      518 FGRQHGKKTITTTGETPERFTYIAHQDT-----GRYPGDMIQININFLPVTN 564
QY      563 EBEIKATNPVATERRPGTVAVNFOSSSTDPAIGDVHAMGALPGMWQDRDYILOGPIMAKI 622
Db      565 DNVLPIPIPIG-----GKTGINV--TNINFTYGLPLALNNVP-----PVPNGQIWDKE 611
QY      623 PHTDGHFHPSPLMGFGGLK-----NPPQILIKNTVPVNPAN---PPAEFSATK 666
Db      612 FDTD-----LKPRLVNAPVPCVCONNCPGLFVKLAPNLITBEDPDASANMSR 658
QY      667 PASFITQSTGOVSVEIEMELÖKENSKRNPVEQYTSNVAKSANVDFTVNNGLYTEBRP 726
Db      659 ---LVTYSDFWKKGLVPKAKLRASHHTNPLQOMISIN-----VDNQFNIV-PSN 703
QY      727 IG 728
Db      704 IG 705
```

Search completed: November 23, 2005, 17:44:00
Job time : 29.9904 secs

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CC medicament for the delivery of transgene to a host. The present sequence
CC is an AAV-1 cap protein VP2 which is useful in the production of
CC recombinant viral vector for gene delivery

XX SQ Sequence 599 AA;

Query Match 100.0%; Score 3251; DB 3; Length 599;
Best Local Similarity 100.0%; Pred. No. 1e-253;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPOLGEPATPAA 60
DB 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPOLGEPATPAA 60
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNHCHDSTWLGDRITTTSTRTMALPTNNHLY 120
DB 61 VGPPTMASGGGAPMADNNEGADGVGNASGNHCHDSTWLGDRITTTSTRTMALPTNNHLY 120
QY 121 KOISSASTGASNDNHFGYSTPMGYFDFNRHCHFSRPMQRLINNNMGFRPKRLNFKLF 180
DB 121 KOISSASTGASNDNHFGYSTPMGYFDFNRHCHFSRPMQRLINNNMGFRPKRLNFKLF 180
QY 181 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQCLPPPADVPMIPQYG 240
DB 181 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQCLPPPADVPMIPQYG 240
QY 241 YLTLLNGSQAVGRSSFYCLEYFPQMLRTGNNTFSYFEEVPHFSSYAHQSGLDRLMNP 300
DB 241 YLTLLNGSQAVGRSSFYCLEYFPQMLRTGNNTFSYFEEVPHFSSYAHQSGLDRLMNP 300
QY 301 LIDQYLYLNTQONSGSAQNKDILLFSRGSFAGMSVQPKMLPGPCYRQQRVSKTKTDNN 360
DB 301 LIDQYLYLNTQONSGSAQNKDILLFSRGSFAGMSVQPKMLPGPCYRQQRVSKTKTDNN 360
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDN 420
DB 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDN 420
QY 421 VMITDEEIKATNPVATERFGTVAVNFQSSSTDPATGVAHMGALPGMWQODRDVYLQGP 480
DB 421 VMITDEEIKATNPVATERFGTVAVNFQSSSTDPATGVAHMGALPGMWQODRDVYLQGP 480
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKTTPVANPAPBSATKFAFFITQYSTG 540
DB 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKTTPVANPAPBSATKFAFFITQYSTG 540
QY 541 QVSVEIEMELQKENSKRNPVEVOYTSNYSKASANDVFTVDNNGLYTEPRPIGTRVYLTRPL 599
DB 541 QVSVEIEMELQKENSKRNPVEVOYTSNYSKASANDVFTVDNNGLYTEPRPIGTRVYLTRPL 599
```

RESULT 2

AA71167 standard; protein; 736 AA.

XX AA71167;

XX 08-SEP-2000 (first entry)

XX Adeno-associated virus serotype 1 capsid protein VP1.

XX Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;

XX cap protein; recombinant viral vector; gene delivery; gene therapy;

XX vaccine; transgene; VPI.

XX Adeno-associated virus 1.

XX WO200028061-A2.

XX 18-MAY-2000.

XX 02-NOV-1999; 99WO-US025694.

PR 05-NOV-1998; 98US-0107114P.

XX (UPE-) UNIV PENNSYLVANIA.

XX Wilson JM, Xiao W,

XX WPI; 2000-376571/32.

XX N-PSDB; AAD00772, AAD00777.

XX Novel adeno-associated virus serotype 1 polynucleotide useful for

XX preparation of medicament for delivery of a transgene to a host.

XX Claim 7; Page 87-90; 108pp; English.

CC The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA
CC which is characterized by two inverted terminal repeats (ITR) and open
CC reading frames for rep and capsid (cap) proteins. The rep reading frame
CC encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap
CC reading frame encodes three structural proteins, VP1, VP2 and VP3. The
CC AAV-1 sequence or its fragments particularly ITRs, rep and cap coding
CC regions, are useful in production of recombinant viral vectors for gene
CC delivery. These vectors can be used as gene therapy vectors, vaccine
CC vectors or antisense delivery vectors. The AAV-1 does not induce the
CC formation of neutralizing antibodies specific to any serotype of AAV
CC hence is useful for transforming host cells, and in the preparation of a
CC medicament for the delivery of transgene to a host. The present sequence
CC is an AAV-1 cap protein VP1 which is useful in the production of
CC recombinant viral vector for gene delivery

XX SQ Sequence 736 AA;

Query Match 100.0%; Score 3251; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPOLGEPATPAA 60
DB 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPOLGEPATPAA 197
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNHCHDSTWLGDRITTTSTRTMALPTNNHLY 120
DB 61 VGPPTMASGGGAPMADNNEGADGVGNASGNHCHDSTWLGDRITTTSTRTMALPTNNHLY 257
QY 121 KOISSASTGASNDNHFGYSTPMGYFDFNRHCHFSRPMQRLINNNMGFRPKRLNFKLF 180
DB 121 KOISSASTGASNDNHFGYSTPMGYFDFNRHCHFSRPMQRLINNNMGFRPKRLNFKLF 317
QY 181 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQCLPPPADVPMIPQYG 240
DB 181 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYQLPYVLGSAHQCLPPPADVPMIPQYG 377
QY 241 YLTLLNGSQAVGRSSFYCLEYFPQMLRTGNNTFSYFEEVPHFSSYAHQSGLDRLMNP 300
DB 241 YLTLLNGSQAVGRSSFYCLEYFPQMLRTGNNTFSYFEEVPHFSSYAHQSGLDRLMNP 437
QY 301 LIDQYLYLNTQONSGSAQNKDILLFSRGSFAGMSVQPKMLPGPCYRQQRVSKTKTDNN 360
DB 301 LIDQYLYLNTQONSGSAQNKDILLFSRGSFAGMSVQPKMLPGPCYRQQRVSKTKTDNN 497
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDN 420
DB 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDN 557
QY 421 VMITDEEIKATNPVATERFGTVAVNFQSSSTDPATGVAHMGALPGMWQODRDVYLQGP 480
DB 421 VMITDEEIKATNPVATERFGTVAVNFQSSSTDPATGVAHMGALPGMWQODRDVYLQGP 617
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKTTPVANPAPBSATKFAFFITQYSTG 540
DB 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKTTPVANPAPBSATKFAFFITQYSTG 677
QY 541 QVSVEIEMELQKENSKRNPVEVOYTSNYSKASANDVFTVDNNGLYTEPRPIGTRVYLTRPL 599
DB 541 QVSVEIEMELQKENSKRNPVEVOYTSNYSKASANDVFTVDNNGLYTEPRPIGTRVYLTRPL 599
```

Db 678 QVSVEIEMELQENSKRNPEVOYTSNVAKSANVDFVNNGLYTEPRPIGTRYLTRPL 736

RESULT 3

ABB80232

ID ABB80232 standard; protein; 736 AA.

XX ABB80232;

DT 20-NOV-2003 (first entry)

XX AAV1 vp1 protein.

XX Adeno-associated virus; AAV; serotype 9; rep; cap; vp1; vp2; vp3;

XX splice variant; transgene.

OS Adeno associated virus serotype 1.

PN WO2003052052-A2.

XX 26-JUN-2003.

XX 12-NOV-2002; 2002WO-US033631.

XX 17-DEC-2001; 2001US-0341150P.

XX 05-JUN-2002; 2002US-0386132P.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Gao G, Wilson JM, Alvira M;

DR WPI; 2003-523523/49.

PT New isolated adeno-associated virus (AAV) comprising an AAV9 capsid,
useful for preparing a medicament for delivering a transgene to a cell.

XX Disclosure; Fig 2; 76pp; English.

XX The sequences given in ABB80231-34 represent vp1 proteins derived from
CC various adeno-associated virus (AAV) serotypes. These sequences were used
CC in the scope of the invention for comparison with the cap protein derived
CC from AAV serotype 9. The AAV capsid comprises three proteins vp1, vp2 and
CC vp3, which are alternative splice variants. The AAV or the nucleic acid
CC molecule is useful for preparing a medicament for delivering a transgene
CC to a cell

SQ Sequence 736 AA;

Query Match 100.0%; Score 3251; DB 6; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAGKKRPVQSGPOEPPSSSGICTGQOPAKKRLNFGQTDSSVDPQPLGSPPTPAA 60

Db 138 TAGGKKRPVQSGPOEPPSSSGICTGQOPAKKRLNFGQTDSSVDPQPLGSPPTPAA 197

QY 61 VGPPTAASGGGAPMADNNEGADGVNAGNMHCDSTWLGDRVITTTSTRTALPTYNHLY 120

Db 198 VGPPTAASGGGAPMADNNEGADGVNAGNMHCDSTWLGDRVITTTSTRTALPTYNHLY 257

QY 121 KQISSASTGASNDNHFGYSTPWGYPDFNPFCHGFSFRDQRLINNMWGFPRKLNFKLF 180

Db 258 KQISSASTGASNDNHFGYSTPWGYPDFNPFCHGFSFRDQRLINNMWGFPRKLNFKLF 317

QY 181 NIQVKEVTNDGVTIANNLTSYVQVPSDEYOLPYVLGSAHOGCLPPPADVFMIPQYG 240

Db 318 NIQVKEVTNDGVTIANNLTSYVQVPSDEYOLPYVLGSAHOGCLPPPADVFMIPQYG 377

QY 241 YLTLLNNGSQAVGSSFFCLEYFSPQMLRTGNNTFFSTFPEVPHSSVYAHSSQSLDRLMNP 300

Db 378 YLTLLNNGSQAVGSSFFCLEYFSPQMLRTGNNTFFSTFPEVPHSSVYAHSSQSLDRLMNP 437

QY 301 LIDQYLYLNRTONQSGAONKDLLFSRGSFAGMSVQPKMWLPGPCYRQORVSKTKTDNN 360

Db 438 LIDQYLYLNRTONQSGAONKDLLFSRGSFAGMSVQPKMWLPGPCYRQORVSKTKTDNN 497

QY 361 NSNFTWGAASKYNLNGRESIINPGTAAASHKXDEDEKFFPPMGSVMI FGESAGASTALDN 420

Db 498 NSNFTWGAASKYNLNGRESIINPGTAAASHKXDEDEKFFPPMGSVMI FGESAGASTALDN 557

QY 421 VMITDEEIKATNPVATERFGVAVNPOSSSTDPATGVHAMGALPGWVMDRDVYLQGP 480

Db 558 VMITDEEIKATNPVATERFGVAVNPOSSSTDPATGVHAMGALPGWVMDRDVYLQGP 617

QY 461 IWAKIPHTDGHFHPSPMLMGFGLKAPPOILIKNTVPANPPEFSATKFAFIQYSGT 540

Db 618 IWAKIPHTDGHFHPSPMLMGFGLKAPPOILIKNTVPANPPEFSATKFAFIQYSGT 677

QY 541 QVSVEIEMELQENSKRNPEVOYTSNVAKSANVDFVNNGLYTEPRPIGTRYLTRPL 599

Db 678 QVSVEIEMELQENSKRNPEVOYTSNVAKSANVDFVNNGLYTEPRPIGTRYLTRPL 736

RESULT 4
ABR62762
ID ABR62762 standard; protein; 736 AA.

XX ABR62762;

XX 06-NOV-2003 (first entry)

XX Adeno associated virus 1 capsid protein vp1.

XX AAV; AAV1; capsid; vector; gene therapy; antisense therapy; vaccine.

OS Adeno associated virus.

PN WO2003052051-A2.

XX 26-JUN-2003.

XX 12-NOV-2002; 2002WO-US033630.

XX 17-DEC-2001; 2001US-0341151P.

XX 01-MAY-2002; 2002US-0377133P.

XX 05-JUN-2002; 2002US-0386122P.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Gao G, Wilson JM, Alvira M;

DR WPI; 2003-523522/49.

PT New adeno-associated virus (AAV) comprising an AAV capsid having an amino
acid sequence of AAV8, useful for preparing a medicament for delivery of
a transgene to a cell and for treating cystic fibrosis or hemophilia B.

XX Disclosure; Fig 2A-C; 82pp; English.

XX The present sequence is the protein sequence of the vp1 capsid protein of
CC adeno associated virus serotype 1 (AAV1). The invention provides the
CC nucleic acid and amino acid sequences of novel AAV8 and fragments of
CC these sequences. Each of these fragments may be used in a variety of
CC vector systems and host cells. Among the desirable fragments are the cap
CC proteins, including vp1, vp2, vp3 and hypervariable regions, the rep
CC proteins, including rep78, rep68, rep52 and rep40, and the sequences
CC encoding these proteins. The fragments may be used alone, in combination
CC with other AAV8 sequences or in combination with elements from other AAV
CC or non-AAV viral sequences in the production of recombinant AAV and for
CC use as antisense delivery vectors, gene therapy vectors or vaccine
CC vectors. A claimed molecule comprises a cap protein of a functional AAV
CC rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and
CC AAV6

SQ Sequence 736 AA;

Query Match 100.0%; Score 3251; DB 7; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAPGKRPEVPSQPEBSSSGIGKTGOQPAKKRLNFGQTGDSSEVPDQPLGEPATPAA 60
DB 138 TAPGKRPEVPSQPEBSSSGIGKTGOQPAKKRLNFGQTGDSSEVPDQPLGEPATPAA 197

QY 61 VGPTTMAAGGGAAPMADNNEGADGVGNASGNHCHCSTWLGDRVITTTSTTMAALPTNNHLY 120
DB 198 VGPTTMAAGGGAAPMADNNEGADGVGNASGNHCHCSTWLGDRVITTTSTTMAALPTNNHLY 257

QY 121 KOISSASTGASNDNHFGYSTPWCYGFDEFRFHCHSPRDMQRLINNMGFPKRLNFKL 180
DB 258 KOISSASTGASNDNHFGYSTPWCYGFDEFRFHCHSPRDMQRLINNMGFPKRLNFKL 317

QY 181 NIQVEVTTNDGVTTIANNLSTVOVFSDSYQLPYVLGSAHQGLPPFPADVPMIPQYG 240
DB 318 NIQVEVTTNDGVTTIANNLSTVOVFSDSYQLPYVLGSAHQGLPPFPADVPMIPQYG 377

QY 241 YLTLLNGSQAVGRSSFYCLEYFPPSQMLRTGNPFSTYFEVPRHSSVAHSQSLDRMLNP 300
DB 378 YLTLLNGSQAVGRSSFYCLEYFPPSQMLRTGNPFSTYFEVPRHSSVAHSQSLDRMLNP 437

QY 301 LIDQYLYLNTQONSGSAQNKDLLFSRGSPPAGMSVQPKMWLPGPCYRQQRVSKTKTDNN 360
DB 438 LIDQYLYLNTQONSGSAQNKDLLFSRGSPPAGMSVQPKMWLPGPCYRQQRVSKTKTDNN 497

QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASTALDN 420
DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASTALDN 557

QY 421 VMTDEBEIKATNPATERFGTVAVNFOSSSTDPATGVHAMGALPGVWMDRDVYLOGP 480
DB 558 VMTDEBEIKATNPATERFGTVAVNFOSSSTDPATGVHAMGALPGVWMDRDVYLOGP 617

QY 481 IWAKIPHTDGHFHPBPLMGFGGLKNPPOILLIKNTVPANPAPBSATKFPASFIQYSTG 540
DB 618 IWAKIPHTDGHFHPBPLMGFGGLKNPPOILLIKNTVPANPAPBSATKFPASFIQYSTG 677

QY 541 QVSVEIEMELQKENSKRNPBEVQYTSNYAKSANVDFTVNNGLYTEPRPIGTRYLTRPL 599
DB 678 QVSVEIEMELQKENSKRNPBEVQYTSNYAKSANVDFTVNNGLYTEPRPIGTRYLTRPL 736

RESULT 5
ADE76565
ID ADE76565 standard; protein; 736 AA.
AC ADE76565;
XX
DT 29-JAN-2004 (first entry)
XX
DE Adeno-associated virus (AAV) related protein, SEQ ID No 64.
XX
KM adeno-associated virus; AAV; cytosolic; antipneumatic; antirheumatic;
KM antiarthritic; neuroprotective; antidiabetic; antichyroid;
KM dermatological; antinflammatory; gene therapy; vaccine;
KM hyperproliferative; cancer; psoriasis; autoimmune disease;
KM rheumatoid arthritis; multiple sclerosis; diabetes;
KM autoimmune thyroiditis; scleroderma; Crohn's disease.
XX
OS unidentified.
XX
XX EP1310571-A2.
XX
PD 14-MAY-2003.
XX
PF 12-NOV-2002; 2002EP-00257826.
XX
XX 13-NOV-2001; 2001US-0350607P.
PR 17-DEC-2001; 2001US-034117P.
PR 01-MAY-2002; 2002US-0377066P.

PR 05-JUN-2002; 2002US-0386675P.
XX
XX (USPE-) UNIV PENNSYLVANIA.
XX
PL Gao G, Wilson JM, Alvira M;
XX WPI; 2003-450984/43.
XX
XX
PT Detecting adeno-associated virus sequences in a sample, useful for e.g.
PT preventing or treating hyperproliferative or autoimmune diseases,
PT comprises subjecting a sample having a DNA to amplification via
PT polymerase chain reaction.
XX
PS Disclosure; SEQ ID NO 64; 419bp; English.
XX
CC The invention relates to a novel method for detecting adeno-associated
CC virus (AAV) sequences in a sample, which comprises subjecting a sample
CC containing a DNA to amplification via a polymerase chain reaction (PCR).
CC The AAV sequence have the following activities: cytosolic,
CC antipneumatic, antirheumatic, antidiabetic, neuroprotective,
CC antiarthritic, antichyroid, dermatological, and antinflammatory. The AAV
CC sequence can be used in gene therapy or as part of a vaccine to treat
CC disorders. The method is useful in detecting and/or identifying AAV
CC sequences and isolating novel sequences that are identified. The
CC sequences may be used e.g. for preventing or treating hyperproliferative
CC conditions such as cancers and psoriasis, and other autoimmune diseases
CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
CC thyroiditis, scleroderma or Crohn's disease. This sequence represents an
CC AAV related protein sequence of the invention.
XX
SQ Sequence 736 AA;

Query Match 100.0%; Score 3251; DB 7; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.4e-253;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAPGKRPEVPSQPEBSSSGIGKTGOQPAKKRLNFGQTGDSSEVPDQPLGEPATPAA 60
DB 138 TAPGKRPEVPSQPEBSSSGIGKTGOQPAKKRLNFGQTGDSSEVPDQPLGEPATPAA 197

QY 61 VGPTTMAAGGGAAPMADNNEGADGVGNASGNHCHCSTWLGDRVITTTSTTMAALPTNNHLY 120
DB 198 VGPTTMAAGGGAAPMADNNEGADGVGNASGNHCHCSTWLGDRVITTTSTTMAALPTNNHLY 257

QY 121 KOISSASTGASNDNHFGYSTPWCYGFDEFRFHCHSPRDMQRLINNMGFPKRLNFKL 180
DB 258 KOISSASTGASNDNHFGYSTPWCYGFDEFRFHCHSPRDMQRLINNMGFPKRLNFKL 317

QY 181 NIQVEVTTNDGVTTIANNLSTVOVFSDSYQLPYVLGSAHQGLPPFPADVPMIPQYG 240
DB 318 NIQVEVTTNDGVTTIANNLSTVOVFSDSYQLPYVLGSAHQGLPPFPADVPMIPQYG 377

QY 241 YLTLLNGSQAVGRSSFYCLEYFPPSQMLRTGNPFSTYFEVPRHSSVAHSQSLDRMLNP 300
DB 378 YLTLLNGSQAVGRSSFYCLEYFPPSQMLRTGNPFSTYFEVPRHSSVAHSQSLDRMLNP 437

QY 301 LIDQYLYLNTQONSGSAQNKDLLFSRGSPPAGMSVQPKMWLPGPCYRQQRVSKTKTDNN 360
DB 438 LIDQYLYLNTQONSGSAQNKDLLFSRGSPPAGMSVQPKMWLPGPCYRQQRVSKTKTDNN 497

QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASTALDN 420
DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASTALDN 557

QY 421 VMTDEBEIKATNPATERFGTVAVNFOSSSTDPATGVHAMGALPGVWMDRDVYLOGP 480
DB 558 VMTDEBEIKATNPATERFGTVAVNFOSSSTDPATGVHAMGALPGVWMDRDVYLOGP 617

QY 481 IWAKIPHTDGHFHPBPLMGFGGLKNPPOILLIKNTVPANPAPBSATKFPASFIQYSTG 540
DB 618 IWAKIPHTDGHFHPBPLMGFGGLKNPPOILLIKNTVPANPAPBSATKFPASFIQYSTG 677

QY 541 QVSVEIEMELQKENSKRNPBEVQYTSNYAKSANVDFTVNNGLYTEPRPIGTRYLTRPL 599

Db 678 QVSVEIEMBLQKENSKRNPVEVOYTSNYSKANSANVDTVDNGLYTERPRIGRIYLRPL 736

RESULT 6
ADV70294
ADV70294 standard; protein; 736 AA.

ADV70294;

10-MAR-2005 (first entry)

Primate adeno-associated virus 1 capsid protein VP1.

immunosuppressive; gene therapy; immunogenicity; virus inactivation;
hemophilia; peptic deficiency; galactosemia; phenylketonuria;
Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
atherosclerosis; thrombosis; embolism; Parkinson's disease;
congestive heart failure; cancer; inflammation; immune disorder;
muscular dystrophy; diabetes; VP1.

Adeno-associated virus 1.

MO2004112727-A2.

29-DEC-2004.

21-JUN-2004; 2004MO-US019884.

19-JUN-2003; 2003US-0480395P.

30-APR-2004; 2004US-0567310P.

03-JUN-2004; 2004US-0576501P.

(AVIG-) AVIGEN INC.

Arbetman AE, Colosi P, Lochrie MA, Surosky RT;

WPI; 2005-048755/05.

New mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating e.g. hemophilia.

Example 5; SEQ ID NO 20; 136pp; English.

The invention describes a mutated adeno-associated virus (AAV) capsid

protein that when present in an AAV virion imparts decreased

immunoreactivity to the virion as compared to the corresponding wild-type

virion. Also described are: a polynucleotide encoding the mutated protein

above; a recombinant AAV virion comprising the mutated protein above; and

delivering a recombinant AAV virion to a cell or tissue of a vertebrate

subject. The recombinant AAV virion is useful for delivering a

heterologous nucleic acid molecule to a cell or tissue of a vertebrate

subject, where the protein encoded by the heterologous nucleic acid

molecule is expressed at a level that provides a non-primate, mammalian

AAV capsid protein that when present in an AAV virion imparts decreased

immunoreactivity to the virion as compared to immunoreactivity of primate

AAV-2, and the heterologous nucleic acid molecule, where the heterologous

nucleic acid molecule encodes a therapeutic protein and is operably

linked to control elements capable of directing the in vivo transcripion

and translation of the protein. The protein or the recombinant AAV virion

is useful for treating or preventing a wide variety of disorders such as

hemophilia, glycogen storage deficiency type 1A, peptic deficiency,

galactosemia, phenylketonuria, Crigler-Najjar disease, Gout and Lesch-

Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis,

thrombosis, embolisms, Parkinson's disease, congestive heart failure,

cancer, inflammatory and immune disorders, muscular dystrophies, and

diabetes. This is the amino acid sequence of adeno-associated virus 1

(AAV1) capsid protein VP1.

Sequence 736 AA;

Query Match 100.0%; Score 3251; DB 9; Length 736;
Best Local Similarity 100.0%; Pred. No. 1,4e-253;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAPGKKRPVEQSPQPDSSSGIGKTGOQPAKKRLNFGQDSESVDPDQPLGEPATPA 60

138 TAPGKKRPVEQSPQPDSSSGIGKTGOQPAKKRLNFGQDSESVDPDQPLGEPATPA 197

61 VGPPTMASGGA PMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLY 120

198 VGPPTMASGGA PMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLY 257

121 KOISSASGASNDNYFGSTWGWFPDRFRFHCHSPRDWQMLINNNGFRKRLNFKLP 180

258 KOISSASGASNDNYFGSTWGWFPDRFRFHCHSPRDWQMLINNNGFRKRLNFKLP 317

181 NIQVEKVTNDGVTTIANNLSTVQVFSDEYQLPVLGSAHQGLPPPADVFMIPOYG 240

318 NIQVEKVTNDGVTTIANNLSTVQVFSDEYQLPVLGSAHQGLPPPADVFMIPOYG 377

241 YLTNNNGSQA VGRSSFCLEYPFSQMLRTGNFTFSYTEEVPFHSSVAHSGLDRKNP 300

378 YLTNNNGSQA VGRSSFCLEYPFSQMLRTGNFTFSYTEEVPFHSSVAHSGLDRKNP 437

301 LIDQYLYINRTONOSGAQNKDLLFSRGSPPGMSVQPPKWLPGPCYRQQRVSKTTDNN 360

438 LIDQYLYINRTONOSGAQNKDLLFSRGSPPGMSVQPPKWLPGPCYRQQRVSKTTDNN 497

361 NSNFTMTGASKYNLNGRESIINPGTAMASHKXDEDFPFMSGVMI FGKSSAGASNTALDN 420

498 NSNFTMTGASKYNLNGRESIINPGTAMASHKXDEDFPFMSGVMI FGKSSAGASNTALDN 557

421 WMITDEEIKATNPVATERFGTVAVNFQSSSTDPAIDVHAGALPGMWQDRDVLQGP 480

558 WMITDEEIKATNPVATERFGTVAVNFQSSSTDPAIDVHAGALPGMWQDRDVLQGP 617

481 IMAKIPHTDGHHPSPFLMGFGCLKNPPOILLIKNTVPANPPAEFATKFASTITQYSTG 540

618 IMAKIPHTDGHHPSPFLMGFGCLKNPPOILLIKNTVPANPPAEFATKFASTITQYSTG 677

541 QVSVEIEMBLQKENSKRNPVEVOYTSNYSKANSANVDTVDNGLYTERPRIGRIYLRPL 599

678 QVSVEIEMBLQKENSKRNPVEVOYTSNYSKANSANVDTVDNGLYTERPRIGRIYLRPL 736

RESULT 7

AD227069
ID AD227069 standard; protein; 736 AA.

AD227069;

30-JUN-2005 (first entry)

Adeno-associated virus protein SEQ ID NO 219.

rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
Kw scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
bacterial infection; cancer; ulcerative colitis; antineoplastic;
antirheumatic; neuroprotective; antiinflammatory; antidiabetic;
Kw antipsoriatic; vasotropic; gastrointestinal gen.; hemostatic; anti-HIV;
Kw virucide; antibacterial; cytostatic; antiulcer; dermatological.

Adeno-associated virus.

MO2005033321-A2.

14-APR-2005.

30-SEP-2004; 2004MO-US028817.

30-SEP-2003; 2003US-0508226P.

29-APR-2004; 2004US-0566546P.

```
XX (UTPE-) UNIV PENNSYLVANIA.
PA
XX
XX Wilson JM, Gao G, Alvirra MR, Vandenbergh LH;
XX
XX WPI, 2005-285437/29.
XX
XX New adeno-associated virus (AAV) clade comprising at least three AAV
XX PT members, useful for preventing and/or treating arthritis, multiple
XX PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
XX PT infection and cancer.
XX
XX Disclosure; SEQ ID NO 219; 569pp; English.
XX
XX The invention relates to an adeno-associated virus (AAV) clade comprising
XX CC at least three AAV members, where each member of the AAV clade is
XX CC phylogenetically related as determined using a Neighbor-joining heuristic
XX CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
XX CC correction distance measurement of no more than 0.05. The methods and
XX CC compositions of the present invention are useful for the prevention
XX CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
XX CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
XX CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
XX CC colitis. The present sequence represents the amino acid sequence of an
XX CC adeno-associated virus protein.
XX
XX Sequence 736 AA:
XX
XX Query Match 100.0%; Score 3251; DB 9; Length 736;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-253;
XX Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TAPGKKRPVEBSPQEPDSSSGIGKTGQOPAKKRLNFGQTGDSVDPDQPLGEPATPAA 60
XX
XX 138 TAPGKKRPVEBSPQEPDSSSGIGKTGQOPAKKRLNFGQTGDSVDPDQPLGEPATPAA 197
XX
XX 61 VGPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWMLPTNNHLY 120
XX
XX 198 VGPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWMLPTNNHLY 257
XX
XX 121 KOISSASTGASNDNHFGYSTPMGYFDNRFHCHFSPRDMQRLINNMGFRPKRLNFKLF 180
XX
XX 258 KOISSASTGASNDNHFGYSTPMGYFDNRFHCHFSPRDMQRLINNMGFRPKRLNFKLF 317
XX
XX 181 NIOVEVTTNDGVTITANNLTSTVOVFSDSBYQLPYVLSAHQGLPPPADVFMIPQYG 240
XX
XX 318 NIOVEVTTNDGVTITANNLTSTVOVFSDSBYQLPYVLSAHQGLPPPADVFMIPQYG 377
XX
XX 241 YTLTNGSQAQVGRSSFYCLEYFPSCQMLRTGNNFTSEYEEPFHSSYAHQSGLDRLAMP 300
XX
XX 378 YTLTNGSQAQVGRSSFYCLEYFPSCQMLRTGNNFTSEYEEPFHSSYAHQSGLDRLAMP 437
XX
XX 301 LIDQYLYVINTRTONOSGAQNKDILFSRGSFAGMSVQPPNMLPGPCYRQORVSKTKTDNN 360
XX
XX 438 LIDQYLYVINTRTONOSGAQNKDILFSRGSFAGMSVQPPNMLPGPCYRQORVSKTKTDNN 497
XX
XX 361 NSNFTWTGASKYNLNRRESITINPGTAMASHKXDEDEFFPMSCVMTFGKSAASATLADN 420
XX
XX 498 NSNFTWTGASKYNLNRRESITINPGTAMASHKXDEDEFFPMSCVMTFGKSAASATLADN 557
XX
XX 421 WMTTDEEIKATNPVATERFGTVAVNFQSSSTDPAQDVHAMGALPGMWQDRDYVLTQSP 480
XX
XX 558 WMTTDEEIKATNPVATERFGTVAVNFQSSSTDPAQDVHAMGALPGMWQDRDYVLTQSP 617
XX
XX 481 IMAKIPHTDGHFHPSPFLMGFGKLPKPPQILIKNTVPANPPAEFSATKFAFITQYSTG 540
XX
XX 618 IMAKIPHTDGHFHPSPFLMGFGKLPKPPQILIKNTVPANPPAEFSATKFAFITQYSTG 677
XX
XX 541 QVSVLEIEMLOKENSRRANPEVOYTSNVAKSANVDPDVTUNNGLYTERPRIGRYYLTRPL 599
XX
XX 678 QVSVLEIEMLOKENSRRANPEVOYTSNVAKSANVDPDVTUNNGLYTERPRIGRYYLTRPL 736
XX
XX
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RESULT 8
AD227012
XX ID AD227012 standard; protein: 736 AA.
XX
XX AC AD227012;
XX
XX 30-JUN-2005 (first entry)
XX
XX DE Adeno-associated virus protein SEQ ID NO 162.
XX
XX rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
XX KM scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
XX KM bacterial infection; cancer; ulcerative colitis; antirheumatic;
XX KM antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
XX KM antiparrotic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
XX KM virucide; antibacterial; cytostatic; antitumor; dermatological.
XX
XX OS Adeno-associated virus.
XX
XX PN MO200503321-A2.
XX
XX PD 14-APR-2005.
XX
XX PF 30-SEP-2004; 2004WO-US028917.
XX
XX PR 30-SEP-2003; 2003US-0508226P.
XX
XX PR 29-APR-2004; 2004US-056546P.
XX
XX (UTPE-) UNIV PENNSYLVANIA.
XX
XX Wilson JM, Gao G, Alvirra MR, Vandenbergh LH;
XX
XX WPI, 2005-285437/29.
XX
XX New adeno-associated virus (AAV) clade comprising at least three AAV
XX PT members, useful for preventing and/or treating arthritis, multiple
XX PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
XX PT infection and cancer.
XX
XX Disclosure; SEQ ID NO 162; 569pp; English.
XX
XX The invention relates to an adeno-associated virus (AAV) clade comprising
XX CC at least three AAV members, where each member of the AAV clade is
XX CC phylogenetically related as determined using a Neighbor-joining heuristic
XX CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
XX CC correction distance measurement of no more than 0.05. The methods and
XX CC compositions of the present invention are useful for the prevention
XX CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
XX CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
XX CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
XX CC colitis. The present sequence represents the amino acid sequence of an
XX CC adeno-associated virus protein.
XX
XX Sequence 736 AA:
XX
XX Query Match 100.0%; Score 3251; DB 9; Length 736;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-253;
XX Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TAPGKKRPVEBSPQEPDSSSGIGKTGQOPAKKRLNFGQTGDSVDPDQPLGEPATPAA 60
XX
XX 138 TAPGKKRPVEBSPQEPDSSSGIGKTGQOPAKKRLNFGQTGDSVDPDQPLGEPATPAA 197
XX
XX 61 VGPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWMLPTNNHLY 120
XX
XX 198 VGPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWMLPTNNHLY 257
XX
XX 121 KOISSASTGASNDNHFGYSTPMGYFDNRFHCHFSPRDMQRLINNMGFRPKRLNFKLF 180
XX
XX 258 KOISSASTGASNDNHFGYSTPMGYFDNRFHCHFSPRDMQRLINNMGFRPKRLNFKLF 317
XX
XX 181 NIOVEVTTNDGVTITANNLTSTVOVFSDSBYQLPYVLSAHQGLPPPADVFMIPQYG 240
XX
XX
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Db      318 NIQKEVTNDGVTITANNLTSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPOYG 377
QY      241 YLTNNGSAVGRSSPYCLEYFPSSQMLRTGNNTFSYTEEVPFHSSVAHSQSLDLRLMP 300
Db      378 YLTNNGSAVGRSSPYCLEYFPSSQMLRTGNNTFSYTEEVPFHSSVAHSQSLDLRLMP 437
QY      301 LIDQYLYLNRTQNGSGAQNKDLPFRSGSPAGMSVQPKNWLPGPCYRQORVSKTIDNN 360
Db      438 LIDQYLYLNRTQNGSGAQNKDLPFRSGSPAGMSVQPKNWLPGPCYRQORVSKTIDNN 497
QY      361 NSNFTWTGASKYNLNRRESIINPGTAMASHKDEDEKFFMSGVMIGKESAGASNTALDN 420
Db      498 NSNFTWTGASKYNLNRRESIINPGTAMASHKDEDEKFFMSGVMIGKESAGASNTALDN 557
QY      421 WMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDYHAGALPGMWQDRDYLQGP 480
Db      558 WMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDYHAGALPGMWQDRDYLQGP 617
QY      481 IWAKIPHTDGHFHPSPLMGFGFKNPPOILLIKNTVPANPPEFSATKFASTITQYSTG 540
Db      618 IWAKIPHTDGHFHPSPLMGFGFKNPPOILLIKNTVPANPPEFSATKFASTITQYSTG 677
QY      541 QVSVEIEMELQKENSRRNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGTIRYLRLP 599
Db      678 QVSVEIEMELQKENSRRNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGTIRYLRLP 736

RESULT 9
ADV67506 standard; protein; 735 AA.
ID      ADV67506
XX      XX
AC      ADV67506;
XX      XX
DT      10-MAR-2005 (first entry)
XX      XX
DE      Amino acid sequence of the capsid protein of AAV serotype 1.
XX      XX
KM      antiarteriosclerotic; antilipemic; gene therapy; cholesterol;
KM      apolipoprotein E; apob; apolipoprotein A; apoa; atherosclerosis;
KM      lipoprotein defect; capsid protein.
XX      XX
OS      Adeno-associated virus.
XX      XX
PN      MO2004108922-A2.
XX      XX
PD      16-DEC-2004.
XX      XX
PF      23-APR-2004; 2004MO-US010965.
XX      XX
PR      25-APR-2003; 2003US-0465293P.
XX      XX
PA      (UYPR-) UNIV PENNSYLVANIA.
XX      XX
PI      Rader DJ, Wilson JM;
XX      XX
DR      WPI; 2005-031700/03.
XX      XX
PT      Lowering total cholesterol levels and treating atherosclerosis in a
PT      subject comprises delivering a recombinant adeno-associated virus (AAV)
PT      comprising an AAV serotype capsid protein or a gene encoding human
PT      apolipoprotein E (apoE) or apoA.
XX      XX
PS      Disclosure; SEQ ID NO 4; 699p; English.
XX      XX
CC      The specification describes a method for lowering total cholesterol
CC      levels in a subject. The method comprises delivering to the subject a
CC      recombinant adeno-associated virus (AAV) comprising a gene encoding a
CC      human apolipoprotein E (apoE) or apoA under the control of a regulatory
CC      control sequence which directs expression of the gene. The recombinant
CC      AAV also comprises a capsid protein selected from an AAV serotype (e.g.,
CC      AAV7 or AAV8) which preferentially expresses high levels of transgene in
CC      live. A therapeutically effective amount of apoE or apoA expression is
CC      obtained upon delivery of low dose of AAV. The method of the invention is

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CC useful for lowering total cholesterol levels in a subject, e.g. for
 CC treating atherosclerosis, and for correcting defects in lipoprotein. The
 CC present sequence represents a capsid protein of AAV serotype 1 (AAV1),
 CC which may be used in recombinant AAV vectors of the invention.

SQ Sequence 735 AA;

Query Match 99.9%; Score 3247; DB 9; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.9e-253;
 Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TAPGKKRPVEGSPQEPDSSSGIGKTGQOPAKRLNFGQGDSESYDPQPLGEPPATPA 60
Db      138 TAPGKKRPVEGSPQEPDSSSGIGKTGQOPAKRLNFGQGDSESYDPQPLGEPPATPA 197
QY      61 VGPPTMASGGGAPMADNNEGADGVNAGSNMHCDSITGLDRVITTSRTWALPTNNHL 120
Db      198 VGPPTMASGGGAPMADNNEGADGVNAGSNMHCDSITGLDRVITTSRTWALPTNNHL 257
QY      121 KOISSASTGASNDNHYFGYSTWGYDFEPRFHCHSPRWMORLINNNMGRPRRLNPKLF 180
Db      258 KOISSASTGASNDNHYFGYSTWGYDFEPRFHCHSPRWMORLINNNMGRPRRLNPKLF 317
QY      181 NIQKEVTNDGVTITANNLTSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPOYG 240
Db      318 NIQKEVTNDGVTITANNLTSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPOYG 377
QY      241 YLTNNGSAVGRSSPYCLEYFPSSQMLRTGNNTFSYTEEVPFHSSVAHSQSLDLRLMP 300
Db      378 YLTNNGSAVGRSSPYCLEYFPSSQMLRTGNNTFSYTEEVPFHSSVAHSQSLDLRLMP 437
QY      301 LIDQYLYLNRTQNGSGAQNKDLPFRSGSPAGMSVQPKNWLPGPCYRQORVSKTIDNN 360
Db      438 LIDQYLYLNRTQNGSGAQNKDLPFRSGSPAGMSVQPKNWLPGPCYRQORVSKTIDNN 497
QY      361 NSNFTWTGASKYNLNRRESIINPGTAMASHKDEDEKFFMSGVMIGKESAGASNTALDN 420
Db      498 NSNFTWTGASKYNLNRRESIINPGTAMASHKDEDEKFFMSGVMIGKESAGASNTALDN 557
QY      421 WMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDYHAGALPGMWQDRDYLQGP 480
Db      558 WMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDYHAGALPGMWQDRDYLQGP 617
QY      481 IWAKIPHTDGHFHPSPLMGFGFKNPPOILLIKNTVPANPPEFSATKFASTITQYSTG 540
Db      618 IWAKIPHTDGHFHPSPLMGFGFKNPPOILLIKNTVPANPPEFSATKFASTITQYSTG 677
QY      541 QVSVEIEMELQKENSRRNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGTIRYLRLP 598
Db      678 QVSVEIEMELQKENSRRNPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGTIRYLRLP 735

RESULT 10
ADZ27074 standard; protein; 736 AA.
ID      ADZ27074
XX      XX
AC      ADZ27074;
XX      XX
DT      30-JUN-2005 (first entry)
XX      XX
DE      Adeno-associated virus protein SEQ ID NO 224.
XX      XX
OS      Adeno-associated virus.
XX      XX
PN      MO2005033321-A2.
XX      XX

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PD 14-APR-2005.
 XX 30-SEP-2004; 2004MO-US028817.
 XX 30-SEP-2003; 2003US-0508226P.
 PR 29-APR-2004; 2004US-0566546P.
 XX (UTYPE-) UNIV PENNSYLVANIA.
 PA
 XX Wilson JM, Gao G, Alvirra MR, Vandenberghe LH;
 PI MPI; 2005-285437/29.
 XX
 PT New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.
 XX
 XX Claim 19; SEQ ID NO 224; 569pp; English.
 PS
 CC The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX
 XX Sequence 736 AA;
 SQ

Query Match 99.4%; Score 3233; DB 9; Length 736;
 Best Local Similarity 99.5%; Pred. No. 3.9e-252;
 Matches 596; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRILNFGQTGSESVDPDQPGEPATPAA 60
 DB 138 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRILNFGQTGSESVDPDQPGEPATPAA 197
 QY 61 VGPPTMASGGAGPMAADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTWMLPTNNHLY 120
 DB 198 VGPPTMASGGAGPMAADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTWMLPTNNHLY 257
 QY 121 KOISSASTGASNDNHYFGYSTPWGTFDENRFCHFSPRDWQRLINNNGFRPKRLNFKLF 180
 DB 258 KOISSASTGASNDNHYFGYSTPWGTFDENRFCHFSPRDWQRLINNNGFRPKRLNFKLF 317
 QY 181 NIOVEVTNDGVTTANNLTSTVOYFSPSEYQLPVYLSAQGCLPPRPADVPMIPQY 240
 DB 338 NIOVEVTNDGVTTANNLTSTVOYFSPSEYQLPVYLSAQGCLPPRPADVPMIPQY 377
 QY 241 YLTINNGSAVGRSSFFCLEYFSPQMLRTGNNFTESYTFEEVYFHSYAHOSGLRLMWP 300
 DB 378 YLTINNGSAVGRSSFFCLEYFSPQMLRTGNNFTESYTFEEVYFHSYAHOSGLRLMWP 437
 QY 301 LIDQYLYNRTONOGSAQONKDLFSRGS PAKMSVQAPNMLPGPCYRQQRVSKTKTDNN 360
 DB 438 LIDQYLYNRTONOGSAQONKDLFSRGS PAKMSVQAPNMLPGPCYRQQRVSKTKTDNN 497
 QY 361 NNFPTWTGASKYNLNRRESITNPGTAMASHKXDEKFFPMGQVMFGKESAGASTALDN 420
 DB 498 NNFPTWTGASKYNLNRRESITNPGTAMASHKXDEKFFPMGQVMFGKESAGASTALDN 557
 QY 421 WMITDEEIKATNPVATERFGTAAVNFQSSSTDPAQDVHAGALPGMTWQDRDYLQSP 480
 DB 558 WMITDEEIKATNPVATERFGTAAVNFQSSSTDPAQDVHAGALPGMTWQDRDYLQSP 617
 QY 481 IMAKIPHTDGHFHPSPFLMGFGGLKNPPQILIKNTFVPANPPAFSATKFAFTIYQSTG 540
 DB 618 IMAKIPHTDGHFHPSPFLMGFGGLKNPPQILIKNTFVPANPPAFSATKFAFTIYQSTG 677

QY 541 QVSVEIEMELQKENS KKMNPVEQYTSNVAKSANDFTVDNNGLYTERPICTRLYLRPL 599
 DB 678 QVSVEIEMELQKENS KKMNPVEQYTSNVAKSANDFTVDNNGLYTERPICTRLYLRPL 736

RESULT 11
 ID ADZ27007 standard; protein; 736 AA.
 AC
 AC ADZ27007;
 DT
 DT 30-JUN-2005 (first entry)
 XX
 DE Adeno-associated virus protein SEQ ID NO 157.
 XX
 XX
 KW rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 KW scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 KW bacterial infection; cancer; ulcerative colitis; antirheumatic;
 KW antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
 KW antiviral; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
 KW virucide; antibacterial; cytostatic; antiulcer; dermatological.
 XX
 OS Adeno-associated virus.
 PD
 PD WO200503321-A2.
 XX
 PN 14-APR-2005.
 PF
 PF 30-SEP-2004; 2004MO-US028817.
 PR
 PR 30-SEP-2003; 2003US-0508226P.
 XX
 XX 29-APR-2004; 2004US-0566546P.
 XX
 XX (UTYPE-) UNIV PENNSYLVANIA.
 PA
 PI Wilson JM, Gao G, Alvirra MR, Vandenberghe LH;
 XX MPI; 2005-285437/29.
 XX
 DR
 DR MPI; 2005-285437/29.
 XX
 XX
 PT New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.
 XX
 XX Claim 19; SEQ ID NO 157; 569pp; English.
 PS
 CC The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX
 XX Sequence 736 AA;
 SQ

Query Match 99.4%; Score 3230; DB 9; Length 736;
 Best Local Similarity 99.2%; Pred. No. 6.9e-252;
 Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRILNFGQTGSESVDPDQPGEPATPAA 60
 DB 138 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRILNFGQTGSESVDPDQPGEPATPAA 197
 QY 61 VGPPTMASGGAGPMAADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTWMLPTNNHLY 120
 DB 198 VGPPTMASGGAGPMAADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTWMLPTNNHLY 257

QY 121 KOISSASTGASNDNHFGYSTWGYFDNFRFHCHSPRDMORLIINNMGFRPKRLNFKLF 180
DB 258 KOISSSTGASNDNHFGYSTWGYFDNFRFHCHSPRDMORLIINNMGFRPKRLNFKLF 317
QY 181 NIQVEVTTNDGVTTIANNLSTVOVFSSEYQLPYVLGSAHQGLPPPAVPMIPOYG 240
DB 318 NIQVEVTTNDGVTTIANNLSTVOVFSSEYQLPYVLGSAHQGLPPPAVPMIPOYG 377
QY 241 YTLNNGSAVGRSSFFCYCLEYFPPSQMLRTGNFTFSEYEEVPFHSYAHSGSLDLRLMP 300
DB 378 YTLNNGSAVGRSSFFCYCLEYFPPSQMLRTGNFTFSEYEEVPFHSYAHSGSLDLRLMP 437
QY 301 LIDQYLYLNRTONOGSAQONKDLFSGSPAGMSVQPKNWLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQYLYLNRTONOGSAQONKDLFSGSPAGMSVQPKNWLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEFFPMGSMVITGKESAGASNTALDN 420
DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEFFPMGSMVITGKESAGASNTALDN 557
QY 421 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDVHAMGALPGMWODRDVYLQGP 480
DB 558 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDVHAMGALPGMWODRDVYLQGP 617
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNDPPQILIKNTFVPANPAEFSAITKFAFITOYSTG 540
DB 618 IMAKIPHTDGHFHPSPLMGFGGLKNDPPQILIKNTFVPANPAEFSAITKFAFITOYSTG 677
QY 541 QVSVEIEMELQKENSKRANPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRTYLRPL 599
DB 678 QVSVEIEMELQKENSKRANPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRTYLRPL 736

RESULT 12

AD227008 standard; protein; 736 AA.

AD227008;

30-JUN-2005 (first entry)

Adeno-associated virus protein SEQ ID NO 158.

XX rhenumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
XX scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
XX bacterial infection; cancer; ulcerative colitis; antineoplastic;
XX antirheumatic; neutroprotective; antiinflammatory; antidiabetic;
XX antipneumonia; vasodilator; gastroenteric; gen.; hemostatic; anti-HIV;
XX virucide; antibacterial; cytostatic; anticancer; dermatological.

Adeno-associated virus.

MO200503321-A2.

14-APR-2005.

30-SEP-2004; 2004MO-US028817.

30-SEP-2003; 2003JUS-0508226P.

29-APR-2004; 2004US-0566546P.

(UYPE-) UNIV PENNSYLVANIA.

W150N UM, Gao G, Alvira MR, Vandenberghe LH;

WPI; 2005-285437/29.

XX New adeno-associated virus (AAV) clade comprising at least three AAV
XX members, useful for preventing and/or treating arthritis, multiple
XX sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
XX infection and cancer.

Claim 19; SEQ ID NO 158; 569pp; English.

XX The invention relates to an adeno-associated virus (AAV) clade comprising
CC at least three AAV members, where each member of the AAV clade is
CC phylogenetically related as determined using a Neighbor-joining heuristic
CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
CC correction distance measurement of no more than 0.05. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
CC colitis. The present sequence represents the amino acid sequence of an
CC adeno-associated virus protein.

SQ Sequence 736 AA;

Query Match 99.4%; Score 3230; DB 9; Length 736;

Best Local Similarity 99.5%; Pred. No. 6; 9e-252; Indels 0; Gaps 0;

Matches 596; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAPGKKRVEQSPQEPDSSSGIGKTGOQPAKKRLNFGOTGSESVDDPQPLGEPPATPA 60
DB 138 TAPGKKRVEQSPQEPDSSSGIGKTGOQPAKKRLNFGOTGSESVDDPQPLGEPPATPA 197
QY 61 VGPPTMASGGAPMADNNEGADGVGNAGNMHCSTWLGDRVITTTSTRTWALPTNNHLY 120
DB 198 VGPPTMASGGAPMADNNEGADGVGNAGNMHCSTWLGDRVITTTSTRTWALPTNNHLY 257
QY 121 KOISSASTGASNDNHFGYSTWGYFDNFRFHCHSPRDMORLIINNMGFRPKRLNFKLF 180
DB 258 KOISSASTGASNDNHFGYSTWGYFDNFRFHCHSPRDMORLIINNMGFRPKRLNFKLF 317
QY 181 NIQVEVTTNDGVTTIANNLSTVOVFSSEYQLPYVLGSAHQGLPPPAVPMIPOYG 240
DB 318 NIQVEVTTNDGVTTIANNLSTVOVFSSEYQLPYVLGSAHQGLPPPAVPMIPOYG 377
QY 241 YTLNNGSAVGRSSFFCYCLEYFPPSQMLRTGNFTFSEYEEVPFHSYAHSGSLDLRLMP 300
DB 378 YTLNNGSAVGRSSFFCYCLEYFPPSQMLRTGNFTFSEYEEVPFHSYAHSGSLDLRLMP 437
QY 301 LIDQYLYLNRTONOGSAQONKDLFSGSPAGMSVQPKNWLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQYLYLNRTONOGSAQONKDLFSGSPAGMSVQPKNWLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEFFPMGSMVITGKESAGASNTALDN 420
DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEFFPMGSMVITGKESAGASNTALDN 557
QY 421 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDVHAMGALPGMWODRDVYLQGP 480
DB 558 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPAVDVHAMGALPGMWODRDVYLQGP 617
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNDPPQILIKNTFVPANPAEFSAITKFAFITOYSTG 540
DB 618 IMAKIPHTDGHFHPSPLMGFGGLKNDPPQILIKNTFVPANPAEFSAITKFAFITOYSTG 677
QY 541 QVSVEIEMELQKENSKRANPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRTYLRPL 599
DB 678 QVSVEIEMELQKENSKRANPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRTYLRPL 736

RESULT 13
AAB59847 standard; protein; 736 AA.
ID AAB59847
XX AAB59847;
XX
XX 28-MAR-2001 (first entry)
XX
XX AAV6 capsid protein VP1.
XX
XX AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;
XX atherosclerosis; sickle cell anemia; thalassemia;
XX blood clotting disorder; diabetes; capsid protein VP1.

XX Adeno associated virus.
 OS US6156303-A.
 XX
 XX 05-DEC-2000.
 XX
 PF 11-JUN-1997; 97US-00873168.
 XX
 PR 11-JUN-1997; 97US-00873168.
 XX
 XX (UNITW) UNIV WASHINGTON.
 XX
 XX Russell DW, Rutledge EA;
 XX
 DR WPI; 2001-060164/07.
 XX
 XX Adeno-associated virus serotype 6 and viral vector derived from it for
 PT gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
 PT syndrome, sickle cell anemia, thalassemia and diabetes.
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present invention relates to adeno-associated virus serotypes. The
 CC present sequence is capsid protein vpi of one such serotype (AAV6). AAV6
 CC can be used to construct AAV viral vectors for use in gene therapy for a
 CC range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,
 CC sickle cell anaemia, thalassemia, blood clotting disorders and diabetes.
 CC The AAV viral vectors have increased transduction efficiency of a
 CC particular host cell as the AAV virion containing the AAV vector genome
 CC can be modified to express a capsid protein of an AAV serotype that
 CC transduces the selected host cell
 XX
 SO Sequence 736 AA;

Query Match 99.3%; Score 3229; DB 4; Length 736;
 Best Local Similarity 99.2%; Pred. No. 8.3e-252;
 Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAPGKRPVBOGPOBSSSGIGKTGOOPAKKRLNFGQTGSBSVDDPQPLGEBPATPAA 60
 DB 138 TAPGKRPVBOGPOBSSSGIGKTGOOPAKKRLNFGQTGSBSVDDPQPLGEBPATPAA 197
 QY 61 VQPTMASGCGAPMADNNGAGDVGNGAGMHCDSWTGLDRYVITSTRTMAIPTNNHLY 120
 DB 198 VQPTMASGCGAPMADNNGAGDVGNGAGMHCDSWTGLDRYVITSTRTMAIPTNNHLY 257
 QY 121 KOISSASTGASNDNHFGYSTPMGYFDFENRFCHFSPPRDQRLINNNMGFRPKRLNFKLF 180
 DB 258 KOISSASTGASNDNHFGYSTPMGYFDFENRFCHFSPPRDQRLINNNMGFRPKRLNFKLF 317
 QY 181 NIQVEKVTNDGVTTIANMLTSTVOYFNSSEVQLPRVYLGSAHQGLCPRPAPVPMIPQYG 240
 DB 318 NIQVEKVTNDGVTTIANMLTSTVOYFNSSEVQLPRVYLGSAHQGLCPRPAPVPMIPQYG 377
 QY 241 YITLNGSAGVARSFPFCLFEPSPQMLRTGNNTFSYEEVFPFSSYAHQSGLRLNMP 300
 DB 378 YITLNGSAGVARSFPFCLFEPSPQMLRTGNNTFSYEEVFPFSSYAHQSGLRLNMP 437
 QY 301 LIDQYLYLNRTOGSGAQNKDLLFSRGSPPAGMSVQPRNMLPGPCYRQQRVSKTKTDNN 360
 DB 438 LIDQYLYLNRTOGSGAQNKDLLFSRGSPPAGMSVQPRNMLPGPCYRQQRVSKTKTDNN 497
 QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDKDFPFMSGVMI FGKSSASASTALDN 420
 DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDKDFPFMSGVMI FGKSSASASTALDN 557
 QY 421 WITDEEBEIKATNPVATERRGTVAANVFOSSSTDPATGDVHANGALPGMWQORDVYLOOP 480
 DB 558 WITDEEBEIKATNPVATERRGTVAANVFOSSSTDPATGDVHANGALPGMWQORDVYLOOP 617
 QY 481 IWAKIPHDTGHFHPSPILMGFGILKNPPOILLIKNTVPANPAPFASATKPAFITOYSTG 540

DB 618 IWAKIPHDTGHFHPSPILMGFGILKNPPOILLIKNTVPANPAPFASATKPAFITOYSTG 677
 QY 541 QVSVEIEMELQKENSKRKNPEVOYTSNYAKSANDFTVDNNGLTETBPRPIGTRILYTRPL 599
 DB 678 QVSVEIEMELQKENSKRKNPEVOYTSNYAKSANDFTVDNNGLTETBPRPIGTRILYTRPL 736

RESULT 14
 ADE76566
 ID ADE76566 standard; protein; 736 AA.
 AC
 AC ADE76566;
 XX
 DT 29-JAN-2004 (first entry)
 XX

DE Adeno-associated virus (AAV) related protein, SEQ ID No 65.

XX adeno-associated virus; AAV; cytosolic; antiproliferative; antineoplastic;
 KW antiarthritic; neuroprotective; antidiabetic; antithyroid;
 KW dermatological; antiinflammatory; gene therapy; vaccine;
 KW hyperproliferative; cancer; psoriasis; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; diabetes;
 KW autoimmune thyroiditis; scleroderma; Crohn's disease.

XX Unidentified.

XX EP310571-A2.

XX 14-MAY-2003.

XX 12-NOV-2002; 2002EP-00257826.

XX 13-NOV-2001; 2001US-0350607P.

XX 17-DEC-2001; 2001US-0341117P.

XX 01-MAY-2002; 2002US-0377066P.

XX 05-JUN-2002; 2002US-0386675P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Gao G, Wilson JM, Alvira M;

XX WPI; 2003-450984/43.

XX Detecting adeno-associated virus sequences in a sample, useful for e.g.
 PT preventing or treating hyperproliferative or autoimmune diseases,
 PT comprises subjecting a sample having a DNA to amplification via
 PT polymerase chain reaction.

XX Disclosure; SEQ ID NO 65; 419pp; English.

XX The invention relates to a novel method for detecting adeno-associated
 CC virus (AAV) sequences in a sample, which comprises subjecting a sample
 CC containing a DNA to amplification via a polymerase chain reaction (PCR).
 CC The AAV sequence have the following activities: cytotoxic,
 CC antiproliferative, antineoplastic, antiarthritic, neuroprotective,
 CC antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV
 CC sequence can be used in gene therapy or as part of a vaccine to treat
 CC disorders. The method is useful in detecting and/or identifying AAV
 CC sequences and isolating novel sequences that are identified. The AAV
 CC sequences may be used e.g. for preventing or treating hyperproliferative
 CC conditions such as cancers and psoriasis, and other autoimmune diseases
 CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
 CC thyroiditis, scleroderma or Crohn's disease. This sequence represents an
 CC AAV related protein sequence of the invention.

XX Sequence 736 AA;

Query Match 99.3%; Score 3229; DB 7; Length 736;
 Best Local Similarity 99.2%; Pred. No. 8.3e-252;
 Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAPGKRPVBOGPOBSSSGIGKTGOOPAKKRLNFGQTGSBSVDDPQPLGEBPATPAA 60
 DB 138 TAPGKRPVBOGPOBSSSGIGKTGOOPAKKRLNFGQTGSBSVDDPQPLGEBPATPAA 197
 QY 61 VQPTMASGCGAPMADNNGAGDVGNGAGMHCDSWTGLDRYVITSTRTMAIPTNNHLY 120
 DB 198 VQPTMASGCGAPMADNNGAGDVGNGAGMHCDSWTGLDRYVITSTRTMAIPTNNHLY 257
 QY 121 KOISSASTGASNDNHFGYSTPMGYFDFENRFCHFSPPRDQRLINNNMGFRPKRLNFKLF 180
 DB 258 KOISSASTGASNDNHFGYSTPMGYFDFENRFCHFSPPRDQRLINNNMGFRPKRLNFKLF 317
 QY 181 NIQVEKVTNDGVTTIANMLTSTVOYFNSSEVQLPRVYLGSAHQGLCPRPAPVPMIPQYG 240
 DB 318 NIQVEKVTNDGVTTIANMLTSTVOYFNSSEVQLPRVYLGSAHQGLCPRPAPVPMIPQYG 377
 QY 241 YITLNGSAGVARSFPFCLFEPSPQMLRTGNNTFSYEEVFPFSSYAHQSGLRLNMP 300
 DB 378 YITLNGSAGVARSFPFCLFEPSPQMLRTGNNTFSYEEVFPFSSYAHQSGLRLNMP 437
 QY 301 LIDQYLYLNRTOGSGAQNKDLLFSRGSPPAGMSVQPRNMLPGPCYRQQRVSKTKTDNN 360
 DB 438 LIDQYLYLNRTOGSGAQNKDLLFSRGSPPAGMSVQPRNMLPGPCYRQQRVSKTKTDNN 497
 QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDKDFPFMSGVMI FGKSSASASTALDN 420
 DB 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDKDFPFMSGVMI FGKSSASASTALDN 557
 QY 421 WITDEEBEIKATNPVATERRGTVAANVFOSSSTDPATGDVHANGALPGMWQORDVYLOOP 480
 DB 558 WITDEEBEIKATNPVATERRGTVAANVFOSSSTDPATGDVHANGALPGMWQORDVYLOOP 617
 QY 481 IWAKIPHDTGHFHPSPILMGFGILKNPPOILLIKNTVPANPAPFASATKPAFITOYSTG 540

DB 138 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGQDSESVDPQPLGEPATPA 197
QY 61 VGPPTMASGGA PMADNNEGADGVNAGSNWCHDSTWLDGRIYITSTRTALPTYNHLY 120
DB 198 VGPPTMASGGA PMADNNEGADGVNAGSNWCHDSTWLDGRIYITSTRTALPTYNHLY 257
QY 121 KOISSASTASNDNHFGYSTWPGYDFNRFHCHSPRPMQRLINNNGFRPRKRLPKLF 180
DB 258 KOISSASTASNDNHFGYSTWPGYDFNRFHCHSPRPMQRLINNNGFRPRKRLPKLF 317
QY 181 NIQVEKVTNDGTTTANNLTSTVOVFSDEYQPLVLSAHQGLPPPADVFMIPQY 240
DB 318 NIQVEKVTNDGTTTANNLTSTVOVFSDEYQPLVLSAHQGLPPPADVFMIPQY 377
QY 241 YLTLLNGSOAVGRSSFYCLEYFPSPQMLRTGNNTFSYTEEVPFHSYAHQSGLDLRLMP 300
DB 378 YLTLLNGSOAVGRSSFYCLEYFPSPQMLRTGNNTFSYTEEVPFHSYAHQSGLDLRLMP 437
QY 301 LIDQVLYLNRITQNGSAQNKDLFSRGS PAMSVQPKWMLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQVLYLNRITQNGSAQNKDLFSRGS PAMSVQPKWMLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYNLNGRSTINGTAMASHKDEDEFPFSGVMTFGKESAGASNTALDN 420
DB 498 NSNFTWTGASKYNLNGRSTINGTAMASHKDEDEFPFSGVMTFGKESAGASNTALDN 557
QY 421 VMTTDEBEIKATNPVATERFGTAVANFOSSSTDPATGDVHAMGALPGMWQDRDYLQGP 480
DB 558 VMTTDEBEIKATNPVATERFGTAVANFOSSSTDPATGDVHAMGALPGMWQDRDYLQGP 617
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILLIKNTVPANPAPAFSATKFASTITQYSTG 540
DB 618 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILLIKNTVPANPAPAFSATKFASTITQYSTG 677
QY 541 QVSVEIEMELQKNSKRNAPDEVQTSYAKSANVDFTVNDNGLYTBRPRIGTYLRLPL 599
DB 678 QVSVEIEMELQKNSKRNAPDEVQTSYAKSANVDFTVNDNGLYTBRPRIGTYLRLPL 736

RESULT 15
ADV70293 ID ADV70293 standard; protein: 736 AA.
XX ADV70293;
AC 10-MAR-2005 (first entry)
DT XX
XX Primate adeno-associated virus 6 capsid protein VP1.
DE XX
XX immunosuppressive; gene therapy; immunogenicity; virus inactivation;
KM hemophilia; Pepck deficiency; galactosemia; phenylketonuria;
KM Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
KM atherosclerosis; thrombosis; embolism; Parkinson's disease;
KM congestive heart failure; cancer; inflammation; immune disorder;
KM muscular dystrophy; diabetes; VPI.
XX
OS Adeno-associated virus 6.
XX
XX WO2004112727-A2.
XX
XX 29-DEC-2004.
XX
XX 21-JUN-2004; 2004WO-US019884.
XX
XX 19-JUN-2003; 2003US-0480395P.
XX 30-APR-2004; 2004US-0567310P.
XX 03-JUN-2004; 2004US-0576501P.
XX
XX (AVIG-) AVIGEN INC.
XX
XX Arbetman AE, Colosi P, Lochrie MA, Surosky RT;
XX
XX WPI; 2005-048755/05.
DR

XX New mutated adeno-associated virus (AAV) capsid protein that when present
PT in an AAV virion imparts decreased immunoreactivity to the virion as
PT compared to the corresponding wild-type virion, useful for treating e.g.
PT hemophilia.
XX
PS Example 5; SEQ ID NO 19; 136pp; English.
XX
CC The invention describes a mutated adeno-associated virus (AAV) capsid
CC protein that when present in an AAV virion imparts decreased
CC immunoreactivity to the virion as compared to the corresponding wild-type
CC virion. Also described are: a polynucleotide encoding the mutated protein
CC above; a recombinant AAV virion comprising the mutated protein above; and
CC delivering a recombinant AAV virion to a cell or tissue of a vertebrate
CC subject. The recombinant AAV virion is useful for delivering a
CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate
CC subject, where the protein encoded by the heterologous nucleic acid
CC molecule is expressed at a level that provides a therapeutic effect,
CC where the recombinant AAV virion may comprise a non-primate, mammalian
CC AAV capsid protein that when present in an AAV virion imparts decreased
CC immunoreactivity to the virion as compared to immunoreactivity of primate
CC AAV-2, and the heterologous nucleic acid molecule, where the heterologous
CC nucleic acid molecule encodes a therapeutic protein and is operably
CC linked to control elements capable of directing the in vivo transcripion
CC and translation of the protein. The protein or the recombinant AAV virion
CC is useful for treating or preventing a wide variety of disorders such as
CC hemophilia, glycogen storage deficiency type Ia, Pepck deficiency,
CC galactosemia, phenylketonuria, Crigler-Najjar disease, Gout and Lesch-
CC Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis,
CC thrombosis, embolisms, Parkinson's disease, congestive heart failure,
CC cancer, inflammatory and immune disorders, muscular dystrophies, and
CC diabetes. This is the amino acid sequence of adeno-associated virus 6
CC (AAV6) capsid protein VP1.
XX
SQ Sequence 736 AA:
Query Match 99.3%; Score 3229; DB 9; Length 736;
Best Local Similarity 99.2%; Pred. No. 8.3e-252;
Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGQDSESVDPQPLGEPATPA 60
DB 138 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGQDSESVDPQPLGEPATPA 197
QY 61 VGPPTMASGGA PMADNNEGADGVNAGSNWCHDSTWLDGRIYITSTRTALPTYNHLY 120
DB 198 VGPPTMASGGA PMADNNEGADGVNAGSNWCHDSTWLDGRIYITSTRTALPTYNHLY 257
QY 121 KOISSASTASNDNHFGYSTWPGYDFNRFHCHSPRPMQRLINNNGFRPRKRLPKLF 180
DB 258 KOISSASTASNDNHFGYSTWPGYDFNRFHCHSPRPMQRLINNNGFRPRKRLPKLF 317
QY 181 NIQVEKVTNDGTTTANNLTSTVOVFSDEYQPLVLSAHQGLPPPADVFMIPQY 240
DB 318 NIQVEKVTNDGTTTANNLTSTVOVFSDEYQPLVLSAHQGLPPPADVFMIPQY 377
QY 241 YLTLLNGSOAVGRSSFYCLEYFPSPQMLRTGNNTFSYTEEVPFHSYAHQSGLDLRLMP 300
DB 378 YLTLLNGSOAVGRSSFYCLEYFPSPQMLRTGNNTFSYTEEVPFHSYAHQSGLDLRLMP 437
QY 301 LIDQVLYLNRITQNGSAQNKDLFSRGS PAMSVQPKWMLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQVLYLNRITQNGSAQNKDLFSRGS PAMSVQPKWMLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYNLNGRSTINGTAMASHKDEDEFPFSGVMTFGKESAGASNTALDN 420
DB 498 NSNFTWTGASKYNLNGRSTINGTAMASHKDEDEFPFSGVMTFGKESAGASNTALDN 557
QY 421 VMTTDEBEIKATNPVATERFGTAVANFOSSSTDPATGDVHAMGALPGMWQDRDYLQGP 480
DB 558 VMTTDEBEIKATNPVATERFGTAVANFOSSSTDPATGDVHAMGALPGMWQDRDYLQGP 617
QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILLIKNTVPANPAPAFSATKFASTITQYSTG 540

Db 618 :
Qy 541
Db 678

Search completed: November 23, 2005, 17:35:12
Job time : 109.044 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 17:29:19 ; Search time 21.1525 Seconds
(without alignment)
2724.684 Million cell updates/sec

Title: US-10-696-282-15

Perfect score: 3251
Sequence: 1 TAPGKRPVEQSPQEPDSSS.....NNGLYTEPRPIGTRIVTRPL 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2177.5	67.0	504	1 VCPV3A	coat protein - ade
2	1701	52.3	732	2 S52210	coat protein VP1 -
3	556	17.1	673	1 VCPVBS	coat protein VP1 -
4	495	15.2	781	1 VCPV19	coat protein VP1 -
5	258.5	8.0	723	1 VCPVPP	coat protein VP1 -
6	254.5	7.8	729	1 A60006	coat protein VP1 -
7	254.5	7.5	729	1 VCPVNA	coat protein VP1 -
8	244	7.2	722	1 VCPV2	coat protein VP1 -
9	234	7.2	587	1 B44276	coat protein VP1 -
10	216	6.6	727	1 VCPV2M	coat protein VP1 -
11	216	6.6	727	1 VCPV1F	coat protein VP1 -
12	214.5	6.6	718	1 VCPV1M	coat protein VP1 -
13	214	6.6	722	1 VCPVME	coat protein VP1 -
14	209	6.4	727	1 VCPVPP	coat protein VP1 -
15	208	6.4	737	1 VCPVCD	coat protein VP1 -
16	204	6.3	748	1 VCPVCP	coat protein VP1 -
17	198	6.1	584	2 S49594	capsid protein VP2
18	192	5.9	722	1 VCPVNC	coat protein VP1 -
19	191	5.9	702	1 VCPVAP	coat protein VP1 -
20	143.5	4.4	648	2 S50856	whn protein - rat
21	129	4.0	1072	2 A86827	hypothetical prote
22	123.5	3.8	690	2 AB0124	probable TonB-depe
23	123	3.8	1142	2 T37455	enamelin precursor
24	122.5	3.7	880	2 SYBSVS	valine-tRNA ligase
25	121	3.7	635	2 F93660	protein F2X11.10
26	121	3.7	1113	2 S28925	nuclear pore compl
27	120.5	3.7	931	2 T49710	related to gluan
28	119	3.7	667	2 A41311	transcription fact
29	118.5	3.6	1180	2 B86719	hypothetical prote

30	118	3.6	739	2 T52289	probable transketo
31	116.5	3.6	642	1 S34416	transcription fact
32	116.5	3.6	1338	2 T30565	MAP kinase kinase
33	115.5	3.6	345	1 G97024	probable phosphoe
34	114	3.5	956	2 T08144	myrosinase-binding
35	114	3.5	2271	2 F90073	hypothetical prote
36	113.5	3.5	2817	2 B97033	uncharacterized pr
37	113	3.5	1071	2 E85343	hypothetical prote
38	112.5	3.5	666	2 T52648	class A helix-loop
39	112.5	3.5	3078	2 T28432	variant-specific B
40	111	3.4	1777	2 T34369	hypothetical prote
41	110.5	3.4	655	1 ALKRG	cyclomaltoextrin
42	110.5	3.4	1742	2 T17120	cellulase (EC 3.2.
43	110	3.4	868	2 A82515	conserved hypothet
44	110	3.4	1296	2 C82521	hemolysin-type cal
45	110	3.4	2825	2 T14271	Doca protein, stre

ALIGNMENTS

RESULT 1

VCPV3A
coat protein - adeno-associated virus type 2

C/Species: adeno-associated virus type 2

C/Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004

C/Accession: A03698

R/Srivastava, A.; Lusby, E.W.; Berns, K.I.

J. Virol. 45, 555-564, 1983

A/Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome.

A/Reference number: A03694; PMID:83164299; PMID:6300419

A/Accession: A03698

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-504 <SRI>

A/Cross-references: UNIPROT:P03135; UNIPARC:UPI0000127C8B; EMBL:J01901; NID:9209616; PIR

C/Superfamily: adeno-associated virus coat protein

C/Keywords: coat protein

Query Match	67.0%	Score	2177.5	DB 1	Length	504			
Best Local Similarity	82.5%	Pred. No.	2.3e-141						
Matches	392	Conservative	33	Mismatches	47	Indels	3	Gaps	2
QY	66	MASGGAPMADNNEGADGCGNAGNHCDSMTLGDRTVITTSRTTWALPTVNNHLYQISS	125						
DB	1	MATGSGAPMADNNEGADGCGNAGNHCDSMTWGDRTVITTSRTTWALPTVNNHLYQISS	60						
QY	126	ASTGASNDNHYPGYSYTPMGYFDPFNRPHCFSPRDMORLNNMGFPRKRLNFKLFINIQVK	185						
DB	61	QS-GASNDNHYPGYSYTPMGYFDPFNRPHCFSPRDMORLNNMGFPRKRLNFKLFINIQVK	119						
QY	186	EVTINDGVTTIANLSTVQVFSDSSEYOLPYVIGSAHQGLPPPADVPMIPOYGYVLTN	245						
DB	120	EVTQNDGTTTIANLSTVQVFTDSEYOLPYVIGSAHQGLPPPADVPMIPOYGYVLTN	179						
QY	246	NSGQAVGRSGFYCLEFPPSQMLRTGNNFTSYFEEVPRFSSVAHSQSILRLNPLIDQY	305						
DB	180	NSGQAVGRSGFYCLEFPPSQMLRTGNNFTSYFEEVPRFSSVAHSQSILRLNPLIDQY	239						
QY	306	LYTLNRTQNGSAGNKKDLFSRGPAGMSVQPKNMLPGCYRQQRSSKTTDNNNSNFT	365						
DB	240	LYTLNRTQNGSAGNKKDLFSRGPAGMSVQPKNMLPGCYRQQRSSKTTDNNNSNFT	299						
QY	366	WTGASKYNLNGRESINPGTAMASHKDDDEKPPMSGVMIFGKESAGASTALDNVMTD	425						
DB	300	WTGATKYNLNGRDSLNVN - AMASHKDDDEKPPMSGVILFGKQSEKTNVNIIEKVMATD	357						
QY	426	EBEIKATNPVATRFGTVAANVPOSSSTDPATGVHAMGALPGVWQDDVDVYLGCPITAKI	485						
DB	358	EBEIGTNPVATRFGTVAANVPOSSSTDPATGVHAMGALPGVWQDDVDVYLGCPITAKI	417						
QY	486	PHDGHFSPPLMGFGCLKNPPQILINRTVPANPAPESATKFAFITQYSTG	540						

DB 418 PHTDGHFHPSPLMGGFGLKHPPLQILIKNTVPANPSTTFSAKAFPTIOYSTG 472

RESULT 2

552210
coat protein VP1 - muscovy duck parvovirus
N:Alternate names: VP1 protein
C:Species: muscovy duck parvovirus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S52210
R:Zadori, Z.; Erdel, J.; Nagy, J.; Kisari, J.
submitted to the EMBL Data Library, September 1993
A:Reference number: S52209
A:Accession: S52210
A:Molecule type: DNA
A:Residues: 1-732 <ZAD>
A:Cross-references: UNIPROT:O83289; UNIPARC:UPI000006C5D; EMBL:X75093; NID:G609091; PIR
A:Experimental source: strain FM
C:Gene: VP1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 52.3%; Score 1701; DB 2; Length 732;
Best Local Similarity 53.0%; Pred. No. 1.6e-108;
Matches 325; Conservative 83; Mismatches 165; Indels 40; Gaps 11;

QY 6 KRPEQSPQEPDSSSGIGK-TGQQPAKKRLNFGQTGDSSEVPDPLG-----E 53
DB 141 EBPVNTAPAKKS---GKLTDDHPVKKPKLSE---ENSPSPNSGGEAATAEGSE 192
QY 54 PATPAVPTTMAAGGAPMADNNGADGVNAGNMHCSTWIGDVTITSTRTMALP 113
DB 193 PVAAP-----NMAEGSGAMGDSAGAGDVGNAAGNMHCDSQWIGDVTITRTWLP 246
QY 114 TNNHLVKOISSASTGASNDNHYFGYSTPMGYFDFNRFCHFSRPMQRLINNMGRPRK 173
DB 247 STNNHMYQAITSGTNPDSN-TQYAGSTPMGYFDFNRFCHFSRPMQRLINNMGRPRK 305
QY 174 RLNFKLFNIOVKVTTNDGVTIANLSTVQVPSDSEVQLPYVLSAHQGLPPRPADV 233
DB 306 ALKFKIFNVQVKEVTTQDQTKTIANNLTSTIQIFTDNEHQLPYVLSAATGTMPPPSDV 365
QY 234 FMIPOGYVTLN---NGSAVGRSSFYCLEFSPQMLRTGNNFTSSYFEERPEPSSVAH 290
DB 366 VALPOGYCTMHTNOSGARFNDRSAYCLEFSPQMLRTGNNFESSFEFEVPEFHSMEFH 425
QY 291 SOSLRINMPLIIDQYLYLNRTQONOSGAQNKDLLFSRGS PAMGSGVQPKMPLPGPCYRQ 350
DB 426 SQDDLRLMPLDQYLYMNSFV-NGGRNQ-----FKKAVKGAFGAMGSMNLPGFKLLDQ 479
QY 351 RVSKTK--TDNNNSNFTWTGASKYNLNGEBSIINPGTAMASHKDEDEKFFPMGVMIRGK 408
DB 480 RYRAVSGGTNDYANMISGKGNKVFLEKDEYLLQPPVATTTHTEDQASSVPAQNIIIGLAK 539
QY 409 E--SAGASNTALDNWITDEERIKAENPYATERFGVAANPOSSSTDPATGVAHMGALP 466
DB 540 DRYRSGSTLAGISDINWTDQELAPTNGVMRPGYGLVTNBOQNTTAPNAELBYVGLAP 599
QY 467 GMYMODRVDYLOGPIWAKIPHTDGHFHPSPLMGGFGLKKNPPOILIKNTVPANPAEFS 526
DB 600 GMYMODRVDYLOGPIWAKIPHTDGHFHPSPLMGGFGLKKNPPOILIKNTVPANPAEFS 659
QY 527 ATKFASPTQYSTGVSEIEMELQKNSKRNREVOYTSNYAKSANDFTVDNNGLYTE 586
DB 660 NQKMSYITQYSTGVSEIEMELQKNSKRNREVOYTSNYAKSANDFTVDNNGLYTE 719
QY 587 PRPIGRYITRP 599
DB 720 DRLIGTRYLTQNL 732

RESULT 3

VCPVB5
coat protein VP1 - bovine parvovirus

N:Contains: coat protein VP2
C:Species: bovine parvovirus
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A26104
R:Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.; Bates, R.C.
J. Virol. 60, 1085-1097, 1986
A:Title: Complete nucleotide sequence and genome organization of bovine parvovirus.
A:Reference number: A26104; MUID:87061184; PMID:3785814
A:Accession: A26104
A:Molecule type: DNA
A:Residues: 1-673 <CHE>
A:Cross-references: UNIPROT:P07297; UNIPARC:UPI0000127D77; EMBL:M14363; NID:G333454; PIR
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:138-673/Product: coat protein VP2 #status predicted <VP2>

Query Match 17.1%; Score 556; DB 1; Length 673;
Best Local Similarity 25.0%; Pred. No. 3.4e-30;
Matches 160; Conservative 98; Mismatches 239; Indels 144; Gaps 19;

QY 1 TAPGKRPEQSPQEPDSSSGIGK-TGQQPAKKRLNFGQTGDSSEVPDPLGEP--PATP 58
DB 100 TSKGDDRALKKKLYFARSNGAKKANREPASTSNQNMVEVNDIPNDEAGNPIELATP 159
QY 59 AAVGPTTMAAGGAPMADNNGADGVNAGNMHCSTWIGDVTITSTRTMALPTVNNH 118
DB 160 SVVSGSVGGGG-----RGSGGVGYSTGWMQGTTFSENIVYTKNTROPICDIXGH 211
QY 119 LYKQISSASTGASNDNHYFGYSTPMGYFDFNRFCHFSRPMQRLINNMGRPRRLNPK 178
DB 212 LYKS-EVANTGDTHARQ-ALTTPMSYFNFGQSHFEPNQMHLVNDYKFRFPAKMLVR 269
QY 179 LENIOVKVTTNDGVTIANL-LTSTVQVPSDSEVQLPYVLSAHQGLPPRPADVEMIP 237
DB 270 VYNIQIKQIMTDGAMGTYYNNDLITAGMHI FCDGHRHYVYQHPMDQCMPELPIWSIWL 329
QY 228 QYGYITL-----NNGSAVGRS-----SFYCLRFSPQMLRTGNNFTFSYTFEEVPHS 286
DB 330 QYAYIPADISVNDNTTWTVEEHLKGVPLYLENSDHEVLNG----- 373
QY 287 SVASQSLRLMNPPLIIDQYLYLNRTQONOSGAQNKDLLFSRGS----- 331
DB 374 -----RKYRIYQIMRLMDKQNHIGHASDVGSTQKQKNNLIQTKQPNKQRF 424
QY 332 AGMSVQPKMPLPGPCYRQVRSKTKTNDNNNSNFTWTGASKYNLNGEBSIINPGTAMASHK 391
DB 425 ONPALRLTNNMNSGP-----GIARGHNTATLOTOSAGALVTWVT 462
QY 392 DDEDEKFFPMGVM-----IFGKE-----SAGASNTALDNWITDE 426
DB 463 NGAD-----VSGVRAVGVSTDPYIGGQPPSDDLRLRYSAAGQGNPTLEN----- 512
QY 427 EIKATNPVATERFGTVAVNFQSSSTDPATGVAHMGALPGMYMODRVDYLOGPIWAKIP 486
DB 513 -----AAKHTFREARITKLIITSGNAGDGYKEMMMLPQNMMSAIPISRNPIIMVAYP 564
QY 487 HTDGHFHPSPLMGGFGLKKNPPOILIK--NTPVPANPAEFSATYFASPTQYSTGVSV 544
DB 565 RVNRKTLTDQDGSIPMSHPTPIFIKLARIIPVGNQ-----SFLNIYVYGVQVSC 615
QY 545 ELEMELQKNSKRNREVOYTSNYAKSAND-FTVDNNGLY 584
DB 616 EVWMEVEKRGTKMREYTHS---ATNMSVAYATTINNAGVY 653

RESULT 4

VCPV19
coat protein VP1 - parvovirus B19 (strain Au)
C:Species: parvovirus B19
A:Note: host Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: A24299
R:Shade, R.O.; Blundell, M.C.; Cotmore, S.F.; Tattersall, P.; Astell, C.R.
J. Virol. 58, 921-936, 1986
A:Title: Nucleotide sequence and genome organization of human parvovirus B19 isolated fr
A:Reference number: A24299; MUID:86200451; PMID:3701931
A:Accession: A24299
A:Molecule type: DNA
A:Residues: 1-781 <SHA>
A:Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; EMBL:ML3178; NID:G333375; PID
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 15.2%; Score 495; DB 1; Length 781;
Best Local Similarity 27.3%; Pred. No. 6.2e-26;
Matches 148; Conservative 84; Mismatches 257; Indels 54; Gaps 16;

```
QY 51 LGEPATPAVPTTMAAGGGA PMADNNGADGVGNAGMHCDSITWLDRTITSTRW 110
DB 213 LREVPAYNSERYSPMTSVNSAB-ASTGAGGGGNSVKSMBEGATFSANVTCTFSKOP 271
QY 111 ALPTYNHLVKOISSASTGASND-----NHYFGYSTPMGYDFENRFCHSPRDM 160
DB 272 LIPYDEHHYKVFSPASSCHNASKGKAVCTISPMGYSTPRYLDFAALMLFESPLDF 331
QY 161 QRLNNMGFRPRKLNFKLNIQVKEVT--TNDGVTIANNLSTVOVFSDBYQLPYVL 218
DB 332 QHLIENYGIADPDLITVISEIAVKQVDTKGGV-QVTDSTTGRLCMLVDHEKYPYVL 390
QY 219 GSAHOGCLPPPADVPMITQYGLTIN- GSOAVG-----RSFYCLEYFSPQMR 268
DB 391 GGGODTLABELPIWYFPPQYALITVGDVNTGIGSDSKLASSESAFYVLEHSSFOLLG 450
QY 269 TGNPFSTFEEVPFHSVAHSQSLDRMLNPLIDQYLYLNRTQNSGSAQNKDLIFSR 328
DB 451 TGTGASMSKTFPPVPEENIEGSGHFEYEMNPL---YGSRLGVPTDLGDPKFRSL----- 503
QY 329 GSPAGNSVOPKMWLPBPCYRQORVSKTKTDNNNSNFTWTGASKRYNLNGEBSIINP- TLM 387
DB 504 -THEDIAIQPNMPPGLVNSVSTKEGDSNTGAKALITGLSTGTSQNTRIISLRPGVQ 562
QY 388 ASHKDEDEKFFPMGSGVMIFGKESAGSNALDNV-----MTDEEIKATNPVATERR 440
DB 563 PYHHWDTDXYVGINAISHGQTTYG---NAEDKEYQGVGRFNEKEQLKLOGLMHTY 619
QY 441 GTAVANFQSSSTDPATGDVYAMGALPGMWQODRDVYLQGPIMAKIPIHTGHHFHS- PLNG 499
DB 620 -----FPNKGITQYTDQIE-RPLMVGSVNRRALHYBSQWSKINLDSFKTQFAALG 672
QY 500 GFGLKNPPQIILKNTPVNPANPPAFESATKFAFITQYSTGVSEIEMEL-QKENSKEW 558
DB 673 GMSLHQPPIQIPLK--ILPQSGPIGGIKSMGITTLVQYAVGIMTVMTFGLGPKATGRW 730
QY 559 NPE 561
DB 731 NPG 733
```

RESULT 5

VCEVPP
coat protein VP1 - porcine parvovirus
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B33302
R:Ranz, A.I.; Mancius, J.J.; Diaz-Aroca, E.; Casael, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A:Title: Porcine parvovirus: DNA sequence and genome organization.
A:Reference number: A33302; MUID:90010964; PMID:2794971
A:Accession: B33302
A:Molecule type: DNA
A:Residues: 1-723 <RAN>
A:Cross-references: UNIPROT:P18546; UNIPARC:UPI0000174964; EMBL:D00623
C:Genetics:

A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:145-723/Product: coat protein VP2 #status predicted <VP2>

Query Match 8.0%; Score 258.5; DB 1; Length 723;
Best Local Similarity 23.1%; Pred. No. 8.6e-10;
Matches 155; Conservative 92; Mismatches 270; Indels 153; Gaps 35;

```
QY 9 VEQSPQEDSSSGIGK-----TGOQPKRLNFGQGDSSGVPDPOPLGEPATP 58
DB 103 VRSPDRKPGSKPCKRPAPRHIFINLAKKAKGTSNTNSMSNENVEOHNDIN--AAE 160
QY 59 -AAVPTTMAAGGGA PMADNNGADGVGNAGMNH--CDSTWLDG--RVITSTRMAL 112
DB 161 LSATNBSGGGGG---GGGAGGVGVSTGSFNNQTEFQYLGGLVITMAHSLRLIHL 216
QY 113 PTYNHLVKOI-----SSASTGAS-NDNHYFGYSTPMGYDFENRFCHSPRDMORLINN 166
DB 217 NMPEHETTKRLIHLNBSGSGAGQVQDDAHQMTPMSLIDANMAGWPNPADMQILSN 276
QY 167 NMGFRPKLNFKLNIQVKEVT--TNDGVTIANNLSTVOVFSDBYQLPYVLGSAHQ 223
DB 277 MTEINLVSPQALFNVLKTTESATSPPTKIYNNDLFASLWALDNTNLTLPYTPAAPS 336
QY 224 GCLPPPADVPMITQYGL-----TLNGSQAVGRSS-----FYCLE-YRP 263
DB 337 ETLGFPYPLPTKPTQYRYLLSCIRNLNPPYTGQSPNNRLNTRLHSDIMEFTIENAVP 396
QY 264 SQMLATQNNF--TFSTFEEVPFHSVAHSQSLDR-----LNNPLI--DOYLYLNRT 312
DB 397 IHLRTRGDEFSTGIYHFDTKPL--KLTHSWQNRSLGLPRLTTEPTTGDDHPTLPAA 454
QY 313 QNQGSAQNKDLIFSRGSPAGNSVOPKMWLPBPCYRQORVSKTKTDNNNSNFTWTGASKY 372
DB 455 NTRKQYHQTINNSYREAT---AIRP-----AQGVYTPMNFESYNGCF 496
QY 373 NLNGEBSIINP--GRAMASHKDEDEKFFPMGSGVMIFGKESAGSNALDNV-----NWMITDBE 427
DB 497 -----LTPVPTADTOYNDDEPN-----CAIRFTMYOHGLHTSSQ 533
QY 428 EIK--ATNP-----VATERFGTVA-VNFOSS-----TDPATG--DVHAMGALP----- 466
DB 534 ELERYTFNPOSKCGRAPKQOFNOQAPLNLNNTNGLTLPBDDIGKSNHFNMTLNTYCP 593
QY 467 -GMVWQODRDVYLQGPIMAKIPIHTD--GHPHSPLMGFGGLK-NPPQIILKNTPVNPANP 522
DB 594 LIALNNTAIPVFPNGQIMDELDLTKPRH---VTAPFVCNNPPQQLFVXIAP---NL 647
QY 523 AEFSA-TKFAFITQYSTGVSEIEMELQKENSKRANPEVOYTSYAKSANDVFTVDNN 581
DB 648 DFNADSPQOPRIITYSNFMWKGTLTFTAKMRSSNMWMDIOHTT-----TAENI 697
QY 582 GLYTPRPYG 591
DB 698 GXYI-PTNIG 706
```

RESULT 6

A60006
coat protein VP1 - porcine parvovirus (strain 90HS)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A60006
R:Sakurai, M.; Nishimori, T.; Uehimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
A:Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A:Reference number: A60006; MUID:89319168; PMID:2750278
A:Accession: A60006
A:Molecule type: DNA
A:Residues: 1-729 <SAK>
A:Cross-references: UNIPROT:P33484; UNIPARC:UPI0000127C6E

C:Species: parvovirus H1
A:Note: host Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C:Accession: A03699
R:Rhode III, S.L.; Parodi, P.R.
J:Virol. 45, 173-184, 1983
A:Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization
A:Reference number: A03695; MUID:83112183; PMID:6823009
A:Accession: A03699
A:Molecule type: DNA
A:Residues: 1-722 <RHO>
A:Cross-references: UNIPROT:P03136; UNIPARC:UPI00001270D; EMBL:X01457; EMBL:J02198
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 7.5%; Score 244; DB 1; Length 722;
Best Local Similarity 21.4%; Pred. No. 8, 4e-09;
Matches 142; Conservative 94; Mismatches 267; Indels 160; Gaps 29;

```
QY      8 PVEQSPQEPDSSSGIGKTGQO---PA-----KKRLNFGQTGDSSEVPDPPLGEP 54
      82 PKLSTDEP-GTSGVSRPGKRTKPRPHITVNGARAKKASLAQOQRLTMSDGTETNP 140
QY      55 PATPAAVGTTMASGGGAPMADNNEGADVGNAAGWCHDSTM--LGDVITTSPTMAL 112
      141 DTGIANARVERSDAGGGS-SGGGSGGGGIGVSTGTVDNQTYYKFGDWVEITAHASRL 199
QY      113 -----PTVNNHLYKQISSASTGASNDNHVFGYSTPMGYDPFNRFCHFSR 158
      200 LHLGMPSENKCVYVHANNOITGHTKVKGNMAVYDHOQIW-TPMSLVANAMGWVFOQS 258
QY      159 DMQRLINNNGWFRPKLNFLENIQVKEVT-----NDGVTTIANLSTVOYFSDSEYO 213
      259 DMQFIQNSMESLNLDSLQELFNVVVKVTEQOQAGADAIKYVNNDLTACMVALDSNNI 318
QY      214 LPLVLSAAGGCL-----PPPAD--VFMIPOGYLTLLNGSQ-----ANG-----R 253
      319 LPLTPAQTSETLGFYPMKPTAPARYYFEMPRQLSVTSSNABEQITDTTIGEPOLAN 378
QY      254 SSFYCLE-YFPSQMLRTGNNFTF-SYTFEEVPFHSVA-----HSQSLDLRAN-PLIDY 305
      379 SQFTLENTLPTLLTGTDEFTTGTIYIFNTDPLKLHTWQTRHNLACLGITDLPFSIDTA 438
QY      306 LLYLNTQNGSGAQNKKDLF-----SRGSPAGMSVOPKMWL 342
      439 TABLTANGDRFGSTQGNVNVYVTEALTRPAQIGFMOPHONFEANGGPKVAVVP---- 494
QY      343 GPCYRQORVSKTKTNNNSNFTWTGASKYNLNGR--ESTLNPCTA-----MASH 390
      495 -----LDITAGEHDHAN--CAIRENYGKHGEEDWAKOGAAPERYTMDAIDSAG 541
QY      391 KQDEDEKFFPMWSGMIKESAGASNTALDNVMTIDESEIKA-TNPVATEKFGTVAVNFOS 449
      542 RDTARACV-----QSAPISIPNQNQIIOREDALAGRNNMHTNVFNSYGPISAF 591
QY      450 SSTDPATGVDHANGALPGWVODRDVYLQGPIMAK--IPHTDGHFHPSPLMGFGGLKNP 506
      592 PHEDP-----LYPQGIWDKELDELHKRPLHTATFV--CKNRP 628
QY      507 PPGILIKNTFVPANPAEF--SATKFSFTIOYSTGOVSVEIEMELQKSKRNPEVOY 564
      629 PGQLFVHLGP---NLTDQFPNSTVSRIVT-YSTFYWKGIKFKAKLRNLTWNPYQA 684
QY      565 TSN 567
      685 TTD 687
DB
```

RESULT 9
B44276
Coat protein VP1 - parvovirus LuIII
C:Species: parvovirus LuIII
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C:Accession: B44276
R:Difford, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-345, 1993
A:Title: The complete nucleotide sequence of parvovirus LuIII and localization of a unit
A:Reference number: B44276; MUID:93297126; PMID:8517025
A:Accession: B44276
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-587 <DIR>
A:Cross-references: UNIPROT:P36310; UNIPARC:UPI00001270E; GB:M81888
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; glycoprotein
F:49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate (Asn) (covalent) #act

Query Match 7.2%; Score 234; DB 1; Length 587;
Best Local Similarity 23.1%; Pred. No. 3e-08;
Matches 137; Conservative 74; Mismatches 231; Indels 152; Gaps 29;

```
QY      59 AAVGPTMASGGGAPMADNNEGADVGNAAGWCHDS--TWLGD--RVITTSPTMAL- 112
      23 AADGPG--GSGGG-----GSGGGGVGVSTGSDNQTHTKFLGDDGWELTAYSTMVHLN 74
QY      113 -PTVNN-----HLKQISSASTGASNDNHVFGYSTPMGYDPFNRFCHFSRDMQRLIN 165
      75 MPKSENYCRVVRHNTNDGTASHMAMDHAQEW-TPMSLVANAMGWVFOQSDWQIYSN 133
QY      166 NNGWFRPKLNFLENIQVKEVT-TNDGVTTIA--NLTSTVOYFSDSEYOPLVLSA 221
      134 NMHINLSLDQELFNVAIKVTEQNTGAEALKVYNNDLTAAWVALDSNNILPTTPAID 193
QY      222 HGGCL-----PPPA-----DVPMIPOGYLTLLNGSOAVGRSSFYCLEYVP 263
      194 NQETLGFYPMKPTLSPYRKYFSCDRNLSTYKDEGITTDTMGLASGLNSQFTIENTQ 253
QY      264 S-QMLRTGNNF-TFSYTFEEVPFHSVAHQSGLRMLPLIDQ-----YL 306
      254 RINLARTGDEVATGYVPTPEIRLHTWQTRHNGQRPQIELPSSDTANATLTARGVR 313
QY      307 VYLNRTQN-----QSGAQNKD-LFSPGSPAGMSVOPKMWLPG----- 344
      314 SGLTQIQGRNDVTEATRVRAQVGFQCPHNDPETSRAQFQVVPADITQIGLHDNAGS 373
QY      345 --PCYRQORVSKTKTNNNSNFTWTGASKYNLNGRESINPTGAMASHDEDEKFPMSG 402
      374 LRYTYDKOHGQSGWASQNNDRYTW-DAVNYD-SGR----- 406
QY      403 VMIFKESAGASNTALDNVMTIDESEIKATNPATER--FGTVAVNFOS--SSTDPATG 457
      407 -----WTNNCFIQSVPTSEPR--ANQILTRDLAKTKTDHFTNANFNSYGPLTA 454
QY      458 DVHANGALPGWVODRDVYLQGPIMAK--IPHTDGHFHPSPLMGFGGLKNPPOILIKN 514
      455 PPH-----PAPIYQGIWDKELDELHKRPLHTQAFV--CKNNAFGQLLVRL 500
QY      515 TP--VPANPAEFAKFSFTIOYSTGOVSVEIEMELQKSKRNPEVOYS 566
      501 APMLTDQYDPSNNSIRIVTGYTFPWKGLTLKAK--MRPVA-TWNPVFOISA 550
DB
```

RESULT 10
VCPV2M
Coat protein VP1 - minute virus of mice
C:Species: minute virus of mice, murine parvovirus
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C:Accession: A03700
R:Atwell, C.R.; Thomson, M.; Merchinsky, M.; Ward, D.C.
Nucleic Acids Res. 11, 999-1018, 1983
A:Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A:Reference number: A03696; MUID:83143341; PMID:6298737
A:Molecule type: DNA
A:Residues: 1-716 <AST>
A:Cross-references: UNIPROT:P03137; UNIPARC:UPI00001270D; EMBL:V01115

C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 6.6%; Score 216; DB 1; Length 716;

Best Local Similarity 20.8%; Pred. No. 6.9e-07;
Matches 148; Conservative 93; Mismatches 271; Indels 198; Gaps 34;

```

QY 8 PVESGQPEPSSSG:GKGTG-----QQPAKKRL-----NFGQT-GDSRSVDP 48
DB 82 PLATDSEB-GTSGVSRACKRTTPRAYIFINQARAKKLTSSAQQSSQTSBDSGPS 140
QY 49 QPLGEPRA--TPAAVPTTMAAGGA PMADNNEGADVGNAGNWHGDS--TWLGD--R 101
DB 141 GNAVSAARVERAADQPG--GSGGG-----GSGGGGVSTGTSVDNQTHRYFLGDGWE 192
QY 102 VTTTSTRTALPTYNHLYKQI-----SSASTGASDNHIFGYSTPMGYDFRFRCH 154
DB 193 ITALATRLVHLMPKSENYCRIRVHTTDTSTYKGNMADDAHQIWTPLSLVDANAGW 252
QY 155 PGRPMQRLINNMGPRKRLNPKLFNIOVKEVTND---GVTTIANLSTVQVPSDS 210
DB 253 LQPSDQYICNTMSQNLVSLDQEIFNVVLKTVTEODLGGQAIKIYNNDLTCMMVAVDS 312
QY 211 EYOLPYVLSAHQGLPPPADVFMIPQYGY-----LTIANSGQAV-----G 252
DB 313 NNILPYTPAANGMETLGFYPMKPTIASPYRYFCVDRDLSTYENQEGTVEHNWGTGK 372
QY 253 RSSEFCLEYFPG-QMLRTGNMF-TFSYTFEEVPHSSVHQSGLDRLMN--PLIDQYLYX 308
DB 373 IPQFFIENTOOITLLRTGDEBFGATGYTFTNSV--KLTHWTQTRKOLQAPLSTF-- 427
QY 309 LMRTONQSGAQNKDLLFSGSPAGMSVQPKML-----PG 344
DB 428 -BEADTDACT-----LTQSGSRHGTTOGGMVWVSEALITRAQVGFQCPHNDFAASRAG 480
QY 345 PCYQROQRVSKTITDNNNSFTWTGASKYMLNGRESIIINGP-----TAMASHKDE 394
DB 481 P-FAAPKVPADITQGVDRKANGSVRSYQKQHEGEMASHGAPARERTYMETSFSGGRDTK 539
QY 395 DXF-----PMSGVMI FGKESAGASNTALDNMTDEBEIKATNPVATBERGTYAV 445
DB 540 DGFISAPLVPPPLNGI-----LTNANPDIQTKN-----DI 570
QY 446 NFGS--SSTDPTAGDVHAMGALPGMWODRDVYLQSPIMAK---IPHTDGHHPRLMG 500
DB 571 HFSNVFNISGPIATASH-----PSVYPOQQLWDXELDEHKRRLHITPAFV-- 617
QY 501 FGLKNPPQILIKNTP--VPANPPAFSATKPFASFTQYSTGVSVIEIEMELQENSKRM 558
DB 618 -CKNNAFGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGLTMRAKLRA-----NTTW 672
QY 559 NBEVQTSYAKSANDVFTVNNGLY---TEPRPIGT-----RYLTRPL 599
DB 673 NBYQVYSAE-----DNGNSYMSYTKMLPFTATGNMOSVPLITREV 711

```

RESULT 11

VCPVIF

coat protein VP1 - feline panleukopenia virus

N:Contains: coat protein VP2

C:Species: feline panleukopenia virus, PFLV

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A03701

R/Caribon, U.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.

J. Virol. 55, 574-587, 1985

A>Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv

A:Reference number: A03697; MUID:85265017; PMID:2991581

A:Accession: A03701

A:Molecule type: DNA

A:Residues: 1-727 <CAR>

A:Cross-references: UNIPROT: P04864; UNIPARC: UP10000127D55; EMBL: M10824; NID: G333474; PID

C:Genetics:

A: Introns: 11/1

C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

F:144-727/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.6%; Score 216; DB 1; Length 727;

Best Local Similarity 20.2%; Pred. No. 7e-07;
Matches 139; Conservative 101; Mismatches 259; Indels 188; Gaps 34;

```

QY 7 RPEQSPQEPSSSG:GKGTGQPAKKRLNFGQTDSSVP-----DQPLGEPRA--TPAA 60
DB 110 KPTRSKPPPHIFINLAK-----KKAAGAQVKRDNQAPMSDQAVDPDGGQAVRNERA 163
QY 61 VGPPTMAAGGAPADNNEGADVGNAGNWHGDS-----CDSTWLGDRVITSTRTALP 113
DB 164 TQSGNAGGCGG-----CGSGGVGISTGTETNNQTEPFLENGWV--EITANSSRLVTLN 215
QY 114 TYNHLYKQI-----SSASTGASDNHIFGYSTPMGYDFRFRCHFSRDMQRLINN 166
DB 216 MPESENYRKYVNNMDTAVKGNMADDTVHQVITPMSLVANAGWVFNPGDQQLVNT 275
QY 167 NMGRPRKRLNPKLFNIOVKEVT---TNDGVTTIANLSTVQVPSDSEYOLPYVLSAHQ 223
DB 276 MSELHVSFEQELFNVLKTVSBSATQPPKVVNNDLTASLMLVLDSTNTTPTPAAKRS 335
QY 224 GCL-----PFPRA-----DVFMIPQYGYLTIANSGQAVGRS-----SFYCL 259
DB 336 ETLGFYPMKPTIIPPMKRYFPQMDRLTLPSh-----TGTSTPTNIYHGTDPDDVQFYTI 389
QY 260 E-YPPSQMLRTGNMF-TFSYTFEEVPHSSVHQSGLDRLMN--PLIDQYLYNRTONO 315
DB 390 ENSVPVHLRTGDEFGATGFFFDCKP--CRLTHWTQTRKALGLRP-----PLNSLPQS 440
QY 316 SGSAQNKDLLFSGSPAGMS-----VQPKN-MLPGCYRQQRYSK----- 354
DB 441 EGATNFGDIGVQOQRRKRVTOGNTDYITEATTIRKPEVGSAPYSEASTQGFKPI 500
QY 355 -----TKTDNNNSFTWTGASKY--NLNGRESIIINGT-----AMASHKDEDKFPMS 401
DB 501 AARGGAQTDENQAA---DQDPRYAFGRHQKQKTTTGETBERFTYLAHQDT----- 549
QY 402 GVMIFGKESAGASNTALD-NMTTDEBEIKATNPVATBERGTYAVNFQSSSTDPAITGVH 460
DB 550 -----GRYPADWTONINFNLPTNDVNLPTDIDIG---GKTGINY--TNIPTYTGPLT 598
QY 461 AMGALPGMWODRDVYLGPIIMAKTIPHTDGHFHSPLMGSGGLK-----NRP 507
DB 599 ALANVP-----PYPNGQIMDXEFTD-----LKRLLHVAAPFCQNNCP 638
QY 508 PQLIKNTPVAN--PPAEFSATKPFASFTQYSTGVSVIEIEMELQENSKRMNPEVQY 564
DB 639 GQLFVKVAPNLITNEVDPPASANMR---IYTGDFPMWKGKLVFPAKLRASHHTNPPIQM 694
QY 565 TSNYAKSANDVFTVNNGLYTPRPIG 591
DB 695 SIN-----VDNQFNYL-PNNIG 710

```

RESULT 12

VCPVIM

coat protein VP1 - minute virus of mice (strain MMV1)

C:Species: minute virus of mice, murine parvovirus

C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: B23008; B29510

R/Saali, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A>Title: DNA sequence comparison between two tissue-specific variants of the autonomous

A:Reference number: A23008; MUID:85242059; PMID:3855242

A:Accession: B23008

A:Molecule type: DNA

A:Residues: 1-718 <SAH>

A:Cross-references: UNIPROT: P07302; UNIPARC: UP10000174963; EMBL: X02481; NID: G60918; PID

C:Genetics: R. Saali, C.R. Gardiner, E.M.; Tattersall, P.

J. Virol. 57, 656-669, 1986

A>Title: DNA sequence of the lymphotropic variant of minute virus of mice, VMV(i), and c
 A:Reference number: A29510; MUID:86115415; PMID:3502703
 A:Accession: B29510
 A:Molecule type: DNA
 A:Residues: 1-143, 'A', 145-718 <AST>
 A:Cross-references: UNIPARC:UPI000012726C; EMBL:M12032
 C:Superfamily: parvovirus coat protein
 C:Keywords: coat protein

Query Match 6.6%; Score 214.5; DB 1; Length 718;
 Best Local Similarity 21.0%; Pred. No. 8.7e-07;
 Matches 142; Conservative 89; Mismatches 273; Indels 171; Gaps 30;

```

      8 PVEQSPQEPDSSSGICKTG-----QQPAKKRLNFG--QTGSESVDPQPLG 52
      83 PKLATSEF-GTSGVSRAGKRTPRAYIFINQARAKKLTSSAAQSSQSTGTSQPDG 141
      53 -----EPPTPAVGPPTTMASGGAPMADNNEGADGVNAGSNHCHDS--TWLGD--R 101
      142 GNGVHSAAVERAADPG--GSGGG-----GSGGGGVGVSTGSYNQTHYRPLDGMWE 193
      102 VITTSRTMALPTYNHLYKQI-----SSASTGASNDNHFGYSTPMGYPENRPHCH 154
      194 ITALATRLVHLNPKSENYCRIVHNTTDTSVKGNMAKODAEQITPMSLVDAWAGW 253
      155 FSPRDQORLINNMGRPKRLNFKLPNIQVEVTND---GYTTIANMLTSTVQVPSDS 210
      254 LQPSDQYICNTMSQJLNVSLDOEIFNVVLKVTBEDSGGQAIKINNLDLTACMWAVDS 313
      211 EYQLPYVLGSAHQCLPPFPADVFMIPQGY-----LTLNN-----GSAQV 251
      314 NNILPTPAANSMETLGFYPMKPTIASPYRYFCVDRLSVTYENQEGTIEHNMVGTSPK 373
      252 GRSFPCLEFPFS-QMLRTGNMF-TSYTFEEVPHSSVHAGSLDLNMF--PLIQOYLX 307
      374 MNSQFTEIENTQITLLRTGDEFAITGYTFDTNPV--KLTHWQTNKQLQPLPLSTF-- 429
      308 YLNRTOGSGSAONKDLFSRGSFAGMSVQPKMWL-----P 343
      430 --PEADTDACT-----LTAQSSRHGATOMEVWVMSAIIETRPAYQFCQPHNFEASRA 481
      344 GPCTYRQORVSKTIDNNNSNFTWTGASKYNLNGRESIINPGTMAHSHKDEDF----- 397
      482 GP-FAAPKVPAVDYQGVDRBANGSVRSYKQKHGEMMAHGPABERYTMBETFGSGRDT 540
      398 ---FPMGSMVIFKESAGSANTALDNMTDEBEIKATNPVATERPETAIVNFQS--SST 452
      541 RDGFTOSAPLVVPPPLNGILTNA-----NPIGTKN---DIHFSNVFNSTY 581
      453 DPATGVDVHMGALPGMWQDRDYYLQGPIMAK--IPHTDGHFHPSPLMGFGFLKPPQP 509
      582 GPLTAPSH-----PSPIYPOQIWDKELDLHKRRLHITAFV--CKNNAHQ 627
      510 ILIKNTP--VPANPPAFSATKFASTIYQSTGVSEIEMWELQENSKRMNPEVOYTSN 567
      628 MVLRLGNLIDQVDPNGATLSRIVTYGTFFWKGLTWRAKLRA---NTWMNPYQQ----- 679
      QY 568 YAKSANVDFTVDNNG 582
      Db 680 -----VSVEDNG 686
  
```

RESULT 13

VCVPWF
 coat protein VP1 - mink entericis virus (strain Abasbiri)
 N:Contains: coat protein VP2
 C:Species: mink entericis virus, MEV
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: B38350
 R:Kariatsunari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishiguro, N.; Goto, H.; Shing
 J. Gen. Virol. 72, 867-875, 1991
 A>Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the
 A:Reference number: A38350; MUID:91202123; PMID:2016597

A:Accession: B38350
 A:Molecule type: DNA
 A:Residues: 1-722 <KAR>
 A:Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
 C:Superfamily: parvovirus coat protein
 C:Keywords: coat protein
 F:139-722/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.6%; Score 214; DB 1; Length 722;
 Best Local Similarity 20.2%; Pred. No. 9.5e-07;
 Matches 139; Conservative 101; Mismatches 259; Indels 188; Gaps 34;

```

      7 PVEQSPQEPDSSSGICKTGQPAKKRLNFGQTGSESV---DPPGLSEPA--TPAA 60
      105 KPTKRSKPPHIFINLAK-----KKKAGGVKRDNLAPMSDGVVDPGGGPAVRNENA 158
      61 VGPPTMASGGAPMADNNEGADGVNAGSNHCHDS--CSTWLGDVRYITSTRTWALP 113
      159 TSSGNGSGGGG-----GGSGGVGISTGTFTNNQTEPFKLENGWV--ETANSSRLVHLN 210
      114 TYNHLYKQI-----SSASTGASNDNHFGYSTPMGYPENRPHCHFSPPDKORLINN 166
      211 MPSENYKRVVNNMDKTAVKGNMALDPTHVQIVTPMSLVDAWAGWENFPGWOLIVNT 270
      167 NMGFPRKRLNFKLPNIQVEVT---TNDGVTTIANMLTSTVQVPSDSEYQLPYVLSAHQ 223
      271 MSELHLVSPFEOEIFNVVLKTVSESATQPPTKVYNNDLTASLWALDSNNTMPTPAKMS 330
      224 GCL-----PPPPA-----DVFMIPOGYLTLNNGSAQVGRS-----SFYCL 259
      331 ETLGTFPMKPTIPTPMKRYFQMDRLILPSH-----TGTSGPTNIYHGTDDDDVFTYI 384
      260 E-YFSPQMLRTGNMF-TSYTFEEVPHSSVHAGSLDLNMF--PLIDOLLYLNRTOHQ 315
      385 ENSVPVHLRLTGDDEFAITGFDFDKP--CRLTHWQTNKQLQPLPLSTF-----FLNGLPOS 435
      316 GSGAONKDLFSRGSFAGMS-----VQPKN-WLQGPCRQORVSK----- 354
      436 EGAITNFGDIGVODKRRGVTQMGNTDYITEATIMRAEVGSAVPSFESTQGPRTPI 495
      355 -----TKTDNNNSNFTWTGASKY--NLNGRESIINPGT---AMASHKDEDEKFPMS 401
      496 AAGRGGAQIDENQAA---DGDRPYAFGRHQGCKTTTGTGTPREFTYIANQDT----- 544
      402 GVMIFKESAGSANTALD-NVMTDEBEIKATNPVATERPFGVAVNVFQSSSTDPAVDH 460
      545 -----GRYPAGDWIQININFLPVTNDVLLPTDPIG---GKTGINY--TINFYTGPILT 593
      461 AMGALPGMWQDRDYYLQGPIMAKIHTDGHFHPSPLMGFGFLK-----NPP 507
      594 ALNNVP-----PVPYPOQIWDKELDLHKRRLHITAFV--CKNNAHQ 633
      508 POLIKNTPVAN--PPAFSATKFASTIYQSTGVSEIEMWELQENSKRMNPEVOY 564
      634 GOLFTVAPALNTNEYDPDASAMNSR---LYTSDPMWKGLVFKKLAASHNTNLIQOM 689
      QY 565 TSNYAKSANVDFTVDNNGLYTEBRPIG 591
      Db 690 SIN-----VDNQFNYL--PNNIG 705
  
```

RESULT 14

VCVPWF
 coat protein VP1 - feline panleukopenia virus (strain 193)
 N:Contains: coat protein VP2
 C:Species: feline panleukopenia virus, FPLV
 C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: B36608
 R:Marlyn, J.C.; Davidson, B.E.; Studdert, M.J.
 J. Gen. Virol. 71, 2747-2753, 1990
 A>Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parv
 A:Reference number: A36608; MUID:91073139; PMID:2174965
 A:Accession: B36608

A: Molecule type: DNA
A: Residues: 1-727 <MAR>
A: Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C: Superfamily: parvovirus coat protein
C: Keywords: coat protein
F: 144-727/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.4%; Score 209; DB 1; Length 727;
Best Local Similarity 20.1%; Pred. No. 2,1e-06;
Matches 138; Conservative 101; Mismatches 260; Indels 188; Gaps 34;

```
QY 7 RPEQSPQEPDSSGIGKTGQQAQKRLNFQGTDSSEVP---DPQLGEPPA--TPAA 60
DB 110 KPTKRSKPPHIFINLAK-----KKKAGAGQVRDNLAPMSDAVQPDGQPAVRNERA 163
QY 61 VGPPTMASGGGAPMADNNEGADGVGNAGSNMH-----CDSTWLGDRVITTSRTYALP 113
DB 164 TGSNGSGGGG-----GGSGGAGVIGTGTNNQTEKFLGKLV--ETANSSRLVHLN 215
QY 114 TYNHLYKQI-----SSASTGASNDNHFGYSTPMGYFDFNRHCHFSPRDMQRLINN 166
DB 216 MPESENTRRVYVNNMDKTAIVGNMALLDIIHQIVTPMSLVDAWAGVWPNFGDQQLIVNT 275
QY 167 NMGFRPKRLNFKLENIQVEKVT--TNDGVTIANNLTSVQVPSDSEYQLPYVLSAHQ 223
DB 276 MSELHLVSFEQEIFNVVLKTVSBSATQPTKVVNNDLTASIMVALDSNNTWFTPAAMRS 335
QY 224 GCL-----PPPPA-----DVFMIPOGYLTLNNGSAVGRS-----SPCYL 259
DB 336 ETLGTFYPMKPTIPTPMRWYFQMDRTLIPSH-----TGTSGPTVIYHGTDDVDVQFTTI 389
QY 260 E-YFPQMLRTGNF--TFSTYFEEVPFHSVAHSQSLDRLMN--PLIDQYLYLNRTONQ 315
DB 390 ENSVPHILRTGDFATGTFPFDCRP--CRLLHTWQTRALGLRP-----FLNSLPQS 440
QY 316 SGSAQNKDLLFSRGSPPAGMS-----VQPKN-WLPGCYRQORVSK-----354
DB 441 EGATNFGDIQVQODKRRGVTQMGNTDYITBATIMRPAEYGSAPYSEFASTQGFPTPI 500
QY 355 -----TKTDNNNSNFTWGASKY---NLNGRESIINPOT---AMASHKDEDEFFMS 401
DB 501 AARGGAQTDENQA--DGDPRVAFGRHQKQTTTGTETPERFYIAHDT-----549
QY 402 GVMIFGKESAGASNTALD-NVMIIDEEIKATNPATERFGTVAVNFQSSSTDPAGDVH 460
DB 550 -----GRYEGDMQININFLPVINDNVLPLTDPIG---GKTGINY--TNIFNYPPLT 598
QY 461 AMGALPGMVMQDRDYVLLQSPITWAKIPHTDGHFHSPLMGFGFLK-----NPP 507
DB 599 ALNNVP-----PYYPNGQIMDKEDTD-----LKPRLHVNAPFVQNNCP 638
QY 508 PQILIKNTFPVPA--PPAFSATKFAFIYQSTGVSEIEMWLOKENSRRNPEVQY 564
DB 639 GQLPFAVAPNLITNEYDPPASAMSR---ITVYSDPMWKGKLVFAKLRASHHTMPIOQ 694
QY 565 TSNVAKSANVDFTVNNGLYTEPRPIG 591
DB 695 SIN-----VDNQFNYYV-PNNIG 710
```

RESULT 15

VC: coat protein VP1 - canine parvovirus (strain CPV-D)
N: Contains: coat protein VP2
C: Species: canine parvovirus, CPV
C: Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C: Accession: A31163
R: Parish, C.R.; Aguadro, C.F.; Carmichael, L.E.
V: Virology 166, 293-307, 1988
A: Title: Canine host range and a specific epitope map along with variant sequences in the
A: Accession: A31163; NID: 89020796; PMID: 3176341
A: Molecule type: DNA

A: Residues: 1-737 <PAR>
A: Cross-references: UNIPROT:P17455; UNIPARC:UPI0000127D7A; EMBL:M23255; NID:G333467; PID
C: Genetics:
A: Introns: 26/3
C: Superfamily: parvovirus coat protein
C: Keywords: coat protein
F: 1584-737/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.4%; Score 208; DB 1; Length 737;
Best Local Similarity 19.8%; Pred. No. 2,5e-06;
Matches 137; Conservative 96; Mismatches 260; Indels 200; Gaps 31;

```
QY 7 RPEQSPQEPDSSGIGKTGQQAQKRLNFQGTDSSEVP---DPQLGEPPA--TPAA 60
DB 120 KPTKRSKPPHIFINLAK-----KKKAGAGQVRDNLAPMSDAVQPDGQPAVRNERA 173
QY 61 VGPPTMASGGGAPMADNNEGADGVGNAGSNMH-----CDSTWLGDRVITTSRTYALP 113
DB 174 TGSNGSGGGG-----GGSGGAGVIGTGTNNQTEKFLGKLV--ETANSSRLVHLN 225
QY 114 TYNHLYKQI-----SSASTGASNDNHFGYSTPMGYFDFNRHCHFSPRDMQRLINN 166
DB 226 MPESENTRRVYVNNMDKTAIVGNMALLDIIHQIVTPMSLVDAWAGVWPNFGDQQLIVNT 285
QY 167 NMGFRPKRLNFKLENIQVEKVT--TNDGVTIANNLTSVQVPSDSEYQLPYVLSAHQ 223
DB 286 MSELHLVSFEQEIFNVVLKTVSBSATQPTKVVNNDLTASIMVALDSNNTWFTPAAMRS 345
QY 224 GCL-----PPPPA-----DVFMIPOGYLTLNNGSAVGRS-----SPCYL 259
DB 346 ETLGTFYPMKPTIPTPMRWYFQMDRTLIPSH-----TGTSGPTVIYHGTDDVDVQFTTI 399
QY 260 E-YFPQMLRTGNF--TFSTYFEEVPFHSVAHSQSLDRLMN--PLIDQYLYLNRTONQ 315
DB 400 ENSVPHILRTGDFATGTFPFDCRP--CRLLHTWQTRALGLRP-----FLNSLPQS 450
QY 316 SGSAQNKDLLFSRGSPPAGMSVQPKNWLPGCYRQORVSKTTDNNNSNF-----TW 366
DB 451 EGATNFGDI-----GV-----QODKRGVTVQMGNTNYITBATIMRPAE 488
QY 367 TGASKYLNNGRESIINP-----GTAMASHKDEDEFFMSVMI-FGKESAGASNTALD-- 419
DB 489 VGYSAPYYSFBSAQGPPEKTPIAARGGAQTDENQAADGNRVAFGHQKQTTTGTETP 548
QY 420 -----NVMIIDEEIKATNPATERFGTVAVNFQSSSTDP 454
DB 549 ERFYIAHQDGRYEGDMQININFLPVINDNVLPLTDPIG---GKTGINY--TNIFN 602
QY 455 ATGDVHAMGALPGMVMQDRDYVLLQSPITWAKIPHTDGHFHSPLMGFGFLK-----504
DB 603 TYGPIITLNNVP-----PYYPNGQIMDKEDTD-----LKPRLHVNAPFV 642
QY 508 PQILIKNTFPVPA--PPAFSATKFAFIYQSTGVSEIEMWLOKENSRRNPEVQY 568
DB 643 CQNNCPQGLFVKVAPNLITNEYDPPASAMSR---ITVYSDPMWKGKLVFAKLRASHHTM 698
QY 565 NPEVQTSNVAKSANVDFTVNNGLYTEPRPIG 591
DB 699 NPIOQMSIN-----VDNQFNYYV-PSNIG 720
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Search completed: November 23, 2005, 17:44:02
Job time: 23.1525 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 17:25:34 ; Search time 115.377 Seconds
(without alignments)
3662.868 Million cell updates/sec

Title: US-10-696-282-15
Score: 3251
Sequence: 1 TAPGKKRPVEQSPQEPDSSS.....NNGLYTEPRPIGTRYLRPL 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3251	100.0	736	2	Q9WB88_VIRU
2	3230	99.4	736	2	Q6JC08_VIRU
3	3230	99.4	736	2	Q6JC12_VIRU
4	3229	99.3	736	2	Q56137_VIRU
5	3203	98.5	736	2	Q6JC10_VIRU
6	3163.5	97.3	737	2	Q6JC13_VIRU
7	2832	87.1	736	2	Q56139_VIRU
8	2831.5	86.8	735	2	Q67008_VIRU
9	2821.5	86.8	735	2	Q6JC28_VIRU
10	2820.5	86.8	735	2	Q6JC34_VIRU
11	2818.5	86.7	735	2	Q6JB21_VIRU
12	2818.5	86.7	735	2	Q6JB27_VIRU
13	2815	86.6	736	2	Q65311_VIRU
14	2808.5	86.4	735	2	Q6JC17_VIRU
15	2807.5	86.4	735	2	Q6JC38_VIRU
16	2807.5	86.4	735	2	Q6JC42_VIRU
17	2803.5	86.2	735	2	Q6JC44_VIRU
18	2802.5	86.2	735	2	Q6JC36_VIRU
19	2800	86.1	734	2	Q6JC02_VIRU
20	2798	86.1	734	2	Q6JC04_VIRU
21	2796.5	86.0	735	2	Q6JB26_VIRU
22	2789.5	85.8	735	2	Q6JC43_VIRU
23	2785.5	85.7	735	2	Q6JB20_VIRU
24	2784.5	85.7	735	2	Q6JB25_VIRU
25	2782.5	85.6	735	2	Q67004_VIRU
26	2781	85.5	734	2	Q6JC03_VIRU
27	2778.5	85.5	735	2	Q67080_VIRU
28	2777.5	85.4	735	2	Q67006_VIRU
29	2775.5	85.4	735	2	Q67008_VIRU
30	2775.5	85.4	735	2	Q6JC41_VIRU
31	2773.5	85.3	735	2	Q67007_VIRU

32	2773.5	85.3	735	2	Q6JC29_VIRU	Q6JC29 adeno-ssoc
33	2771.5	85.3	735	2	Q6JC39_VIRU	Q6JC39 adeno-ssoc
34	2769.5	85.2	735	2	Q67006_VIRU	Q67006 adeno-ssoc
35	2768.5	85.2	735	2	Q67008_VIRU	Q67008 adeno-ssoc
36	2766.5	85.1	735	2	Q6JC25_VIRU	Q6JC25 adeno-ssoc
37	2766.5	85.1	736	2	Q6JC24_VIRU	Q6JC24 adeno-ssoc
38	2764.5	85.0	735	2	Q56652_AAV2	Q56652 adeno-ssoc
39	2764.5	85.0	735	2	Q6JC31_VIRU	Q6JC31 adeno-ssoc
40	2763.5	85.0	735	2	Q6JC01_VIRU	Q6JC01 adeno-ssoc
41	2763.5	85.0	735	2	Q6JC35_VIRU	Q6JC35 adeno-ssoc
42	2761.5	84.9	735	2	Q68089_VIRU	Q68089 non-human p
43	2759.5	84.9	598	2	Q56653_AAV2	Q56653 adeno-ssoc
44	2759.5	84.9	735	2	Q6JB24_VIRU	Q6JB24 adeno-ssoc
45	2758.5	84.9	735	2	Q6JC26_VIRU	Q6JC26 adeno-ssoc

ALIGNMENTS

RESULT 1	Q9WB88_VIRU	PRELIMINARY;	PRT;	736 AA.
AC	Q9WB88;			
DT	01-NOV-1999 (Tremblrel. 12, Created)			
DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Capid protein.			
OS	Adeno-associated virus 1.			
OC	Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.			
OX	NCBI_TaxID=85106;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=9921438; PubMed=10196295;			
RA	Xiao W., Chirmule N., Barta S.C., McCullough B., Gao G., Wilson J.M.;			
RT	"Gene therapy vectors based on adeno-associated virus type 1."			
RL	J. Virol. 73:3994-4003(1999).			
DR	EMBL; AF063497; AAD2757.1; -; Genomic_DNA.			
DR	SMR; Q9WB88; 217-736.			
DR	GO; GO:0019028; C:viral capsid; IEA.			
DR	GO; GO:0005198; P:structural molecule activity; IEA.			
DR	InterPro; IPR001403; Parvo coat.			
DR	Pfam; PF00740; Parvo coat; 1.			
SQ	SEQUENCE 736 AA; 81375 MW; CFABFB9BDS00595 CRC64;			
Query Match	100.0%; Score 3251; DB 2; Length 736;			
Best local Similarity	100.0%; Pred. No. 5.1e-216;			
Matches	599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 TAPGKKRPVEQSPQEPDSSSGIGTGGQPAKKRLNCGTGSSEVPDPQLGEPATPPA 60			
DB	138 TAPGKKRPVEQSPQEPDSSSGIGTGGQPAKKRLNCGTGSSEVPDPQLGEPATPPA 197			
QY	61 VPTTASGCGAPMADNNEGADGVNAGSNMHCSTWLGDRIYITSTRMALPTYNHL 120			
DB	198 VPTTASGCGAPMADNNEGADGVNAGSNMHCSTWLGDRIYITSTRMALPTYNHL 257			
QY	121 KQISSASTGASNDNHFGYSTPWGYFDENRFCHESPRDWRLINNMGFRPRGLNFKLF 180			
DB	258 KQISSASTGASNDNHFGYSTPWGYFDENRFCHESPRDWRLINNMGFRPRGLNFKLF 317			
QY	181 NIOVKAVTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHOGCLPPPADVFMIPQY 240			
DB	318 NIOVKAVTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHOGCLPPPADVFMIPQY 377			
QY	241 YLTINNGSAQVGRSFFCYLEFPQMLRTGNFTFSYTEEVPFHSVYAHSGSLDLRLMP 300			
DB	378 YLTINNGSAQVGRSFFCYLEFPQMLRTGNFTFSYTEEVPFHSVYAHSGSLDLRLMP 437			
QY	301 LIDQVLYLNRITQNGSAGQNKDLFSSRSPAGMSVQPKMLPGPCYRQORVSKTIDNN 360			
DB	438 LIDQVLYLNRITQNGSAGQNKDLFSSRSPAGMSVQPKMLPGPCYRQORVSKTIDNN 497			
QY	361 NSNFTTGAASKYVNLNGBESTINPGTAMASHKDEBDFPMSGVMIFGKSAGASNTALDN 420			

|||||
Db NSNFTWTGASKYNLNGRESIIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASTALDN 557
498
Qy 421 VMITDEEBEIKATNPVATERFCTAVANFQSSSTDPAIDGVHMGALPGVMWDDRDVYLQGP 480
421
Db 558 VMITDEEBEIKATNPVATERFCTAVANFQSSSTDPAIDGVHMGALPGVMWDDRDVYLQGP 617
617
Qy 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPOILIKNTPVANPAPFASATKFAFITQYSTG 540
481
Db 618 IMAKIPHTDGHFHPSPLMGFGGLKNPPOILIKNTPVANPAPFASATKFAFITQYSTG 677
618
Qy 541 QVSVEIEMELQKENSKRNPPEVQYTSNVAKSANVDFVNNGLYTEPPRIGTRYLTRPL 599
541
Db 678 QVSVEIEMELQKENSKRNPPEVQYTSNVAKSANVDFVNNGLYTEPPRIGTRYLTRPL 736
678

RESULT 2
Q6JC08_9VIRU
ID Q6JC08_9VIRU PRELIMINARY; PRT; 736 AA.
AC Q6JC08;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Capsid protein Vp1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
Wilson J.M.;
RA "Clades of Adeno-associated viruses are widely disseminated in human
tissues";
RT J. Virol. 78:6381-6388(2004).
RL EMBL; AY530611; AAS99292.1; -; Genomic_DNA.
DR SMR; Q6JC08; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat; 1.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD CRC64;

Query Match 99.4%; Score 3230; DB 2; Length 736;
Best Local Similarity 99.2%; Pred. No. 1.4e-214;
Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TAPGKKRPVEQSPQEPDSSSGIGKTQQPAKKRLNFGQTGDSSEVPDPQPLGEPPTPAA 60
1
Db 138 TAPGKKRPVEQSPQEPDSSSGIGKTQQPAKKRLNFGQTGDSSEVPDPQPLGEPPTPAA 197
138
Qy 61 VGPTTMASSGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTRTMALPTYNNHLY 120
61
Db 198 VGPTTMASSGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTRTMALPTYNNHLY 257
198
Qy 121 KOISSASGASNDNHYFGYSTPMGWFPDNRHCHSPDWMQRLINNMMGFRPKRLNFKLF 180
121
Db 258 KOISSASGASNDNHYFGYSTPMGWFPDNRHCHSPDWMQRLINNMMGFRPKRLNFKLF 317
258
Qy 181 NIQVEVTTNDGVTTIANNLSTVOVFSDSSEYQLPYVLSAHQGLPEFPADVMIPOYG 240
181
Db 318 NIQVEVTTNDGVTTIANNLSTVOVFSDSSEYQLPYVLSAHQGLPEFPADVMIPOYG 377
318
Qy 241 YLTINNGQAVGRSSFYCLEYFPQMLRTGNFTFSYTEEVPHSSYAHQSQSLDRLMNP 300
241
Db 378 YLTINNGQAVGRSSFYCLEYFPQMLRTGNFTFSYTEEVPHSSYAHQSQSLDRLMNP 437
378
Qy 301 LIDQVLYLNTQONSGAQNKDILFSRGSAPGMSVQPKNMLPGPCYRQOVSKTKTDNN 360
301
Db 438 LIDQVLYLNTQONSGAQNKDILFSRGSAPGMSVQPKNMLPGPCYRQOVSKTKTDNN 497
438
Qy 361 NSNFTWTGASKYNLNGRESIIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASTALDN 420
361

|||||
Db NSNFTWTGASKYNLNGRESIIINPGTAVASHKDEDEKFFPMGVMIFGKESAGASTALDN 557
498
Qy 421 VMITDEEBEIKATNPVATERFCTAVANFQSSSTDPAIDGVHMGALPGVMWDDRDVYLQGP 480
421
Db 558 VMITDEEBEIKATNPVATERFCTAVANFQSSSTDPAIDGVHMGALPGVMWDDRDVYLQGP 617
617
Qy 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPOILIKNTPVANPAPFASATKFAFITQYSTG 540
481
Db 618 IMAKIPHTDGHFHPSPLMGFGGLKNPPOILIKNTPVANPAPFASATKFAFITQYSTG 677
618
Qy 541 QVSVEIEMELQKENSKRNPPEVQYTSNVAKSANVDFVNNGLYTEPPRIGTRYLTRPL 599
541
Db 678 QVSVEIEMELQKENSKRNPPEVQYTSNVAKSANVDFVNNGLYTEPPRIGTRYLTRPL 736
678

RESULT 3
Q6JC12_9VIRU
ID Q6JC12_9VIRU PRELIMINARY; PRT; 736 AA.
AC Q6JC12;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Capsid protein Vp1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
Wilson J.M.;
RA "Clades of Adeno-associated viruses are widely disseminated in human
tissues";
RT J. Virol. 78:6381-6388(2004).
RL EMBL; AY530607; AAS99292.1; -; Genomic_DNA.
DR SMR; Q6JC12; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat; 1.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CRC64;

Query Match 99.4%; Score 3230; DB 2; Length 736;
Best Local Similarity 99.5%; Pred. No. 1.4e-214;
Matches 596; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TAPGKKRPVEQSPQEPDSSSGIGKTQQPAKKRLNFGQTGDSSEVPDPQPLGEPPTPAA 60
1
Db 138 TAPGKKRPVEQSPQEPDSSSGIGKTQQPAKKRLNFGQTGDSSEVPDPQPLGEPPTPAA 197
138
Qy 61 VGPTTMASSGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTRTMALPTYNNHLY 120
61
Db 198 VGPTTMASSGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTRTMALPTYNNHLY 257
198
Qy 121 KOISSASGASNDNHYFGYSTPMGWFPDNRHCHSPDWMQRLINNMMGFRPKRLNFKLF 180
121
Db 258 KOISSASGASNDNHYFGYSTPMGWFPDNRHCHSPDWMQRLINNMMGFRPKRLNFKLF 317
258
Qy 181 NIQVEVTTNDGVTTIANNLSTVOVFSDSSEYQLPYVLSAHQGLPEFPADVMIPOYG 240
181
Db 318 NIQVEVTTNDGVTTIANNLSTVOVFSDSSEYQLPYVLSAHQGLPEFPADVMIPOYG 377
318
Qy 241 YLTINNGQAVGRSSFYCLEYFPQMLRTGNFTFSYTEEVPHSSYAHQSQSLDRLMNP 300
241
Db 378 YLTINNGQAVGRSSFYCLEYFPQMLRTGNFTFSYTEEVPHSSYAHQSQSLDRLMNP 437
378
Qy 301 LIDQVLYLNTQONSGAQNKDILFSRGSAPGMSVQPKNMLPGPCYRQOVSKTKTDNN 360
301
Db 438 LIDQVLYLNTQONSGAQNKDILFSRGSAPGMSVQPKNMLPGPCYRQOVSKTKTDNN 497
438
Qy 361 NSNFTWTGASKYNLNGRESIIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASTALDN 420
361

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DB 498 NSNFTWTGASKYLNIGRESIIINPGTAMASHKODEKFFPMGVMIFGKESASASTALDN 557
QY 421 VMITDEEIKATNPVATERFGTVAVNFOSSTDPATGDVHAMGALPGMWODRDVYLOGP 480
DB 558 VMITDEEIKATNPVATERFGTVAVNFOSSTDPATGDVHAMGALPGMWODRDVYLOGP 617
QY 481 IWAKIPHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAEFSATKFSFITYSTG 540
DB 618 IWAKIPHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAEFSATKFSFITYSTG 677
QY 541 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNGLYTEPRPIGTRYLTRPL 599
DB 678 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNGLYTEPRPIGTRYLTRPL 736
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RESULT 4
ID 056137_9VIRU PRELIMINARY; PRT; 736 AA.
AC 056137;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Capsid protein VP1.
OS Adeno-associated virus 6.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=68558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98080418; PubMed=9420229;
RA Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2.";
RL J. Virol. 72:309-319(1998).
DR EMBL; AF028704; AAB95450.1; -; Genomic_DNA.
DR SMR; 056137; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81411 MW; 311217A089C565F5 CRC64;
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Query Match 99.3%; Score 3229; DB 2; Length 736;
Best Local Similarity 99.2%; Pred. No. 1.7e-214;
Matches 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 TAPGKKRPVQSQPOEPPSSSGIGKTGQOPAKKRLNFGQTDSESVDPQPLGSPATPPA 60
DB 138 TAPGKKRPVQSQPOEPPSSSGIGKTGQOPAKKRLNFGQTDSESVDPQPLGSPATPPA 197
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTMALPTYNHLY 120
DB 198 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTMALPTYNHLY 257
QY 121 KQISSASTGASNDNHFGYSTPWGYFDNRFCHFSFRDQORLINNMGFRPKRLNFKLF 180
DB 258 KQISSASTGASNDNHFGYSTPWGYFDNRFCHFSFRDQORLINNMGFRPKRLNFKLF 317
QY 181 NIOVEKVTINDGVTTIANNLITSTYQVFSDESYQLPYVLGSAHQGCLPPFADVFMIPOYG 240
DB 318 NIOVEKVTINDGVTTIANNLITSTYQVFSDESYQLPYVLGSAHQGCLPPFADVFMIPOYG 377
QY 241 YLTLLNNGSOAVGRSSFYCLEYFPSONLRTGNNTFFSYTFEEVPHSSVYAHOSGLDRLAMP 300
DB 378 YLTLLNNGSOAVGRSSFYCLEYFPSONLRTGNNTFFSYTFEEVPHSSVYAHOSGLDRLAMP 437
QY 301 LIDQYLYLNRTQNGSQAQNKDILFSRGSPPAGMSVQPKMWLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQYLYLNRTQNGSQAQNKDILFSRGSPPAGMSVQPKMWLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYLNIGRESIIINPGTAMASHKODEKFFPMGVMIFGKESASASTALDN 420
DB 498 NSNFTWTGASKYLNIGRESIIINPGTAMASHKODEKFFPMGVMIFGKESASASTALDN 557
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QY 421 VMITDEEIKATNPVATERFGTVAVNFOSSTDPATGDVHAMGALPGMWODRDVYLOGP 480
DB 558 VMITDEEIKATNPVATERFGTVAVNFOSSTDPATGDVHAMGALPGMWODRDVYLOGP 617
QY 481 IWAKIPHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAEFSATKFSFITYSTG 540
DB 618 IWAKIPHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAEFSATKFSFITYSTG 677
QY 541 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNGLYTEPRPIGTRYLTRPL 599
DB 678 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNGLYTEPRPIGTRYLTRPL 736
```

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RESULT 5
ID 06JC10_9VIRU PRELIMINARY; PRT; 736 AA.
AC 06JC10;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530609; AAS99294.1; -; Genomic_DNA.
DR SMR; 06JC10; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81388 MW; BA9463B970028DF0 CRC64;
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Query Match 98.8%; Score 3203; DB 2; Length 736;
Best Local Similarity 98.8%; Pred. No. 1.1e-212;
Matches 592; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 TAPGKKRPVQSQPOEPPSSSGIGKTGQOPAKKRLNFGQTDSESVDPQPLGSPATPPA 60
DB 138 TAPGKKRPVQSQPOEPPSSSGIGKTGQOPAKKRLNFGQTDSESVDPQPLGSPATPPA 197
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTMALPTYNHLY 120
DB 198 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTMALPTYNHLY 257
QY 121 KQISSASTGASNDNHFGYSTPWGYFDNRFCHFSFRDQORLINNMGFRPKRLNFKLF 180
DB 258 KQISSASTGASNDNHFGYSTPWGYFDNRFCHFSFRDQORLINNMGFRPKRLNFKLF 317
QY 181 NIOVEKVTINDGVTTIANNLITSTYQVFSDESYQLPYVLGSAHQGCLPPFADVFMIPOYG 240
DB 318 NIOVEKVTINDGVTTIANNLITSTYQVFSDESYQLPYVLGSAHQGCLPPFADVFMIPOYG 377
QY 241 YLTLLNNGSOAVGRSSFYCLEYFPSONLRTGNNTFFSYTFEEVPHSSVYAHOSGLDRLAMP 300
DB 378 YLTLLNNGSOAVGRSSFYCLEYFPSONLRTGNNTFFSYTFEEVPHSSVYAHOSGLDRLAMP 437
QY 301 LIDQYLYLNRTQNGSQAQNKDILFSRGSPPAGMSVQPKMWLPGPCYRQORVSKTKTDNN 360
DB 438 LIDQYLYLNRTQNGSQAQNKDILFSRGSPPAGMSVQPKMWLPGPCYRQORVSKTKTDNN 497
QY 361 NSNFTWTGASKYLNIGRESIIINPGTAMASHKODEKFFPMGVMIFGKESASASTALDN 420
DB 498 NSNFTWTGASKYLNIGRESIIINPGTAMASHKODEKFFPMGVMIFGKESASASTALDN 557
```

```
QY 421 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGMWODRDVYLQGP 480
DB 558 VMTDEEIKATNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGMWODRDVYLQGP 617
QY 481 IWAKIPHTDGHFHPSPLMGFGCLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTG 540
DB 618 IWAKIPHTDGHFHPSPLMGFGCLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTG 677
QY 541 QVSVEIEWELQKENSKRNPPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRYLTRPL 599
DB 678 QVSVEIEWELQKENSKRNPPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRYLTRPL 736
```

RESULT 6

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Q6JC13 9VIRU PRELIMINARY; PRT; 737 AA.
AC Q6JC13;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Capsid protein VPI.
GN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530606; AAS9291.1; -; Genomic_DNA.
DR SMR; Q6JC13; 218-737.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvovir coat.
DR Pfam; PF00740; Parvovir coat; 1.
SQ SEQUENCE 737 AA; 81332 MW; 94CED0F3AFD68492 CRC64;
```

```
Query Match 97.3%; Score 3163.5; DB 2; Length 737;
Best Local Similarity 97.3%; Pred. No. 5.7e-210;
Matches 584; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
```

```
QY 1 TAPGKKRPVEQSPQ-BPDSSSGIGKTGQOPAKKRLNFGQTGDSSEVPDQPIGEPAPTPA 59
DB 138 TAPGKKRPVEQSPQ-BPDSSSGIGKTGQOPAKKRLNFGQTGDSSEVPDQPIGEPAPTPA 197
QY 60 AVGPPTMASGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTMALPTYNNHL 119
DB 198 GAGSGTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTMALPTYNNHL 257
QY 120 YKOISSASTGASNDNHFGYSTPWCYFDNRFHCHFSPPDMQRLINNMGFRPKLNFCLF 179
DB 258 YKOISSASTGASNDNHFGYSTPWCYFDNRFHCHFSPPDMQRLINNMGFRPKLNFCLF 317
QY 180 FNIQVEVTTNDGVTTIANNLTSTVOVFSDESYOLPYVLGSAHQGLPPFPADVPMIPQY 239
DB 318 FNIQVEVTTNDGVTTIANNLTSTVOVFSDESYOLPYVLGSAHQGLPPFPADVPMIPQY 377
QY 240 GYTLTNGSOAVGRSFFCYCLEYFPQMLRTGNNTFTSYTFEEVPHFSYAHQSILDRLLNP 299
DB 378 GYTLTNGSOAVGRSFFCYCLEYFPQMLRTGNNTFTSYTFEEVPHFSYAHQSILDRLLNP 437
QY 300 PLIDQLYLYLNTQNGSGAQNKDLLFSRGSPPAGMSVQPKNMLPGPCYRQORVSKTKTDN 359
DB 438 PLIDQLYLYLNTQNGSGAQNKDLLFSRGSPPAGMSVQPKNMLPGPCYRQORVSKTKTDN 497
QY 360 NNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFPFMGSVMI FGKESAGASNTALD 419
DB 498 NNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFPFMGSVMI FGKESAGASNTALD 557
```

```
QY 420 NVMTDEEIKATNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGMWODRDVYLQGP 479
DB 558 NVMTDEEIKATNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGMWODRDVYLQGP 617
QY 480 PIWAKIPHTDGHFHPSPLMGFGCLKNPPQILIKNTVPANPPAEFSATKFASTITQYST 539
DB 618 PIWAKIPHTDGHFHPSPLMGFGCLKNPPQILIKNTVPANPPAEFSATKFASTITQYST 677
QY 540 QVSVEIEWELQKENSKRNPPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRYLTRPL 599
DB 678 QVSVEIEWELQKENSKRNPPEVOYTSNYAKSANVDFTVNNGLYTEPRPIGRYLTRPL 737
```

RESULT 7

```
Q56139 9VIRU PRELIMINARY; PRT; 736 AA.
AC Q56139;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Capsid protein VPI.
GN Adeno-associated virus 3B.
OS Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=68742;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98080418; PubMed=9420229;
RA Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2.";
RL J. Virol. 72:309-319(1998).
DR EMBL; AF028705; AAB95452.1; -; Genomic_DNA.
DR SMR; Q56139; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvovir coat.
DR Pfam; PF00740; Parvovir coat; 1.
SQ SEQUENCE 736 AA; 81906 MW; DD52331AD5F0D70F CRC64;
```

```
Query Match 87.1%; Score 2832; DB 2; Length 736;
Best Local Similarity 85.7%; Pred. No. 4.8e-187;
Matches 514; Conservative 34; Mismatches 50; Indels 2; Gaps 2;
```

```
QY 1 TAPGKKRPVEQSPQ-BPDSSSGIGKTGQOPAKKRLNFGQTGDSSEVPDQPIGEPAPTPA 60
DB 138 TAPGKKRPVDSQPBPSSSGIGKTGQOPAKKRLNFGQTGDSSEVPDQPIGEPAPTPA 197
QY 61 VGPTTMAAGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTMALPTYNNHL 120
DB 198 LGSNTMASGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTSRTMALPTYNNHL 257
QY 121 KOISSASTGASNDNHFGYSTPWCYFDNRFHCHFSPPDMQRLINNMGFRPKLNFCLF 180
DB 258 KOISSOS-GASNDNHFGYSTPWCYFDNRFHCHFSPPDMQRLINNMGFRPKLNFCLF 316
QY 181 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYOLPYVLGSAHQGLPPFPADVPMIPQY 240
DB 317 NIQVEVTTNDGVTTIANNLTSTVOVFSDESYOLPYVLGSAHQGLPPFPADVPMIPQY 376
QY 241 YTLTNGSOAVGRSFFCYCLEYFPQMLRTGNNTFTSYTFEEVPHFSYAHQSILDRLLNP 300
DB 377 YTLTNGSOAVGRSFFCYCLEYFPQMLRTGNNTFTSYTFEEVPHFSYAHQSILDRLLNP 436
QY 301 LIDQLYLYLNTQ-NQSGAQNKDLLFSRGSPPAGMSVQPKNMLPGPCYRQORVSKTKTDN 359
DB 437 LIDQLYLYLNTQGTGTTNQSRLFSQAPQOSMSLDARWMLPGPCYRQORVSKTKTDN 496
QY 360 NNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFPFMGSVMI FGKESAGASNTALD 419
DB 497 NNSNFTWTGASKYNLNGRESIINPGTAMASHKODEDKFPFMGSVMI FGKESAGASNTALD 556
QY 420 NVMTDEEIKATNPVATERFGTVAVNFQSSSTDPATGVDHAMGALPGMWODRDVYLQGP 479
```

```
Db 557 NMWIDDEEIRTNVATIEQYGVANNLOSSNTAPTRTNOGALPGVWQDRDYVLOG 616
Oy 480 IMAKIPHTDGHFHPBPLMGFGFLKKNPPOIILIKNTVPANPPAEFSATKFASTIYQYST 539
Db 617 IMAKIPHTDGHFHPBPLMGFGFLKKNPPOIILIKNTVPANPPPTTSPAKFASFIYQYST 676
Oy 540 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNNGLYTEPPPIGTRYLTRPL 599
Db 677 QVSVEIEWELQKENSKRNNPEIQTYSNYSKSVNVDFTVDNGVSEPRPIGTRYLTRNL 736
```

RESULT 8
Q67008_VIRU PRELIMINARY; PRT; 735 AA.

```
AC 067008;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chen C.L., Jensen R.L., Schnepp B.C., Connell M.J., Bartlett J.S.,
RA Sferri T.J., Shell R., Johnson P.R., Clark K.R.;
RT "Characterization of Adeno-Associated Viruses in Children.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY695376; AAU05370.1; -; Genomic_DNA.
DR SMR; Q67008; 217-735.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvovir coat.
DR Pfam; PF00740; Parvovir coat.
SQ SEQUENCE 735 AA; 81887 MW; 258BFB955F1C9925 CRC64;
```

Query Match 87.1%; Score 2831.5; DB 2; Length 735;
Best Local Similarity 85.0%; Pred. No. 5.1e-187;
Matches 509; Conservative 39; Mismatches 50; Indels 1; Gaps 1;

```
Oy 1 TAPGKRPVPSQPOEPDSSSGIGKTGQOPAKRLNFGQTSQDSVPDPQPLGEPPTPA 60
Db 138 TAPGKRPVPSHAPEDSSSGTAKSGQOPAKRLNFGQTSQDSVPDPQPLGEPPTPA 197
Oy 61 VGPPTMASGGGAPMADNNEGADGVNAGSGNWHCDSTWLGDRVITSTRTVALPTYNHLY 120
Db 198 LGSTTMAISGAPMADNNEGADGVNAGSGNWHCDSTWLGDRVITSTRTVALPTYNHLY 257
Oy 121 KOISASTGASNDNHFGYSTPWGYFDNRFCHFSPRDMQRLINNMGFRPRKLNFKLF 180
Db 258 KOISASQGS-GASNDNHFGYSTPWGYFDNRFCHFSPRDMQRLINNMGFRPRKLNFKLF 316
Oy 181 NIQVEKVTNDGVTTIANNLSTVQVFSDEYQLPYVLSAHOCCLPFPADVFMIPOYG 240
Db 317 NIQVEKVTNDGVTTIANNLSTVQVFTDSEYQLPYVLSAHOCCLPFPADVFMIPOYG 376
Oy 241 YLTLLNNGSQAAGRSSPYCLEYFSPSOMLRTGNNTFSTFEVYFPHSSVYASOSLDLAMP 300
Db 377 YLTLLNNGSQAAGRSSPYCLEYFSPSOMLRTGNNTFSTFEVYFPHSSVYASOSLDLAMP 436
Oy 301 LIDQVLYLNRQONSGAQNKDLIFSRGSPAGMSVOPKRWLPGPCYRQORVSKTKTDN 360
Db 437 LIDQVLYLNRQONSGAQNKDLIFSRGSPAGMSVOPKRWLPGPCYRQORVSKTKTDN 496
Oy 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FCKESAGASNTALDN 420
Db 497 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FCKESAGASNTALDN 556
Oy 421 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGDVYAMGALPGMWQDRDYVLOG 480
Db 557 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGDVYAMGALPGMWQDRDYVLOG 616
```

```
Oy 481 IMAKIPHTDGHFHPBPLMGFGFLKKNPPOIILIKNTVPANPPAEFSATKFASTIYQYSTG 540
Db 617 IMAKIPHTDGHFHPBPLMGFGFLKKNPPOIILIKNTVPANPPPTTSPAKFASFIYQYSTG 676
Oy 541 QVSVEIEWELQKENSKRNNPEVOYTSNYAKSANDFTVDNNGLYTEPPPIGTRYLTRPL 599
Db 677 QVSVEIEWELQKENSKRNNPEIQTYSNYSKSVNVDFTVDNGVSEPRPIGTRYLTRNL 735
```

RESULT 9
Q6UC28_VIRU PRELIMINARY; PRT; 735 AA.

```
AC 06UC28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530591; AAS9276.1; -; Genomic_DNA.
DR SMR; Q6UC28; 217-735.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvovir coat.
DR Pfam; PF00740; Parvovir coat.
SQ SEQUENCE 735 AA; 81897 MW; 197066F8911FA9B CRC64;
```

Query Match 86.8%; Score 2821.5; DB 2; Length 735;
Best Local Similarity 84.5%; Pred. No. 2.5e-186;
Matches 506; Conservative 40; Mismatches 52; Indels 1; Gaps 1;

```
Oy 1 TAPGKRPVPSQPOEPDSSSGIGKTGQOPAKRLNFGQTSQDSVPDPQPLGEPPTPA 60
Db 138 TAPGKRPVPSHAPEDSSSGTAKSGQOPAKRLNFGQTSQDSVPDPQPLGEPPTPA 197
Oy 61 VGPPTMASGGGAPMADNNEGADGVNAGSGNWHCDSTWLGDRVITSTRTVALPTYNHLY 120
Db 198 LGSTTMAISGAPMADNNEGADGVNAGSGNWHCDSTWLGDRVITSTRTVALPTYNHLY 257
Oy 121 KOISASTGASNDNHFGYSTPWGYFDNRFCHFSPRDMQRLINNMGFRPRKLNFKLF 180
Db 258 KOISASQGS-GASNDNHFGYSTPWGYFDNRFCHFSPRDMQRLINNMGFRPRKLNFKLF 316
Oy 181 NIQVEKVTNDGVTTIANNLSTVQVFSDEYQLPYVLSAHOCCLPFPADVFMIPOYG 240
Db 317 NIQVEKVTNDGVTTIANNLSTVQVFTDSEYQLPYVLSAHOCCLPFPADVFMIPOYG 376
Oy 241 YLTLLNNGSQAAGRSSPYCLEYFSPSOMLRTGNNTFSTFEVYFPHSSVYASOSLDLAMP 300
Db 377 YLTLLNNGSQAAGRSSPYCLEYFSPSOMLRTGNNTFSTFEVYFPHSSVYASOSLDLAMP 436
Oy 301 LIDQVLYLNRQONSGAQNKDLIFSRGSPAGMSVOPKRWLPGPCYRQORVSKTKTDN 360
Db 437 LIDQVLYLNRQONSGAQNKDLIFSRGSPAGMSVOPKRWLPGPCYRQORVSKTKTDN 496
Oy 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FCKESAGASNTALDN 420
Db 497 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FCKESAGASNTALDN 556
Oy 421 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGDVYAMGALPGMWQDRDYVLOG 480
Db 557 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGDVYAMGALPGMWQDRDYVLOG 616
```

```
QY 481 IWAKIPHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPPAPESATKFASTTQYSTG 540
DB 617 IWAKIPHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPPPTNSSAKFASFTQYSTG 676
QY 541 QVSVEIEMELQKENSCKRMNPEVOYTSNYSKANSANDFTVDNNGLYTERPIGTRILTRPL 599
DB 677 QVSVEIEMELQKENSCKRMNPEIQYTSNYSKANSVNDFTVDNNGVSEBRPIGTRILTRNL 735
```

RESULT 10

```
Q6JC34_9VIRU PRELIMINARY; PRT; 735 AA.
ID Q6JC34_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JC34;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Capsid protein VPI.
DE Name=cap;
GN Adeno-associated virus.
OS Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
CX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues."
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530628; AAS99270.1; -; Genomic_DNA.
DR SMR; Q6JC34; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81962 MW; 85DC69C5232D983 CRC64;
```

```
Query Match 86.8%; Score 2820.5; DB 2; Length 735;
Best Local Similarity 84.5%; Pred. No. 3e-166;
Matches 506; Conservative 41; Mismatches 51; Indels 1; Gaps 1;
```

```
QY 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPQIGSEPPATPA 60
DB 138 TAPGKKRPVEHSPVEPDSSSGTGKAGQPARAKRLNFGQTGADSVDPDQIGSEPPAASG 197
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTSRTMALPTYNHLY 120
DB 198 LGSTTMATGSGAPMADNNEGADGVGNASGNMHCDSQMLGDRVITTSRTMALPTYNHLY 257
QY 121 KOISSASTGASNDNHYFGYSTPMGYPDPNRFCHSPRDMQRLINNMGFRPKLNFKLF 180
DB 258 KOISSOS-GASNDNHYFGYSTPMGYPDPNRFCHSPRDMQRLINNMGFRPKLNFKLF 316
QY 181 NIQVEVTTNDGVTIANNLSTVQVFSDESEYQLPYVLGSAHQGLPEPPADVMIPOYG 240
DB 317 NIQVEVTTNDGVTIANNLSTVQVFSDESEYQLPYVLGSAHQGLPEPPADVMIPOYG 376
QY 241 YLTLLNGSAOAVGRSSFYCLEYFPSCMLRTGNFTFSYEEVPFHSSVYAHQSGLDRLNMP 300
DB 377 YLTLLNGSAOAVGRSSFYCLEYFPSCMLRTGNFTFSYEEVPFHSSVYAHQSGLDRLNMP 436
QY 301 LIDQVLYLNTQNSGSAQKDLFSRGSAPGMSVOPKJMLPGPCYRQOQSVSKTKTDNN 360
DB 437 LIDQVLYLNTQNSGSAQKDLFSRGSAPGMSVOPKJMLPGPCYRQOQSVSKTKTDNN 496
QY 361 NSNFTWGTASKYNLNGRESINPGTAMASHKDDKDFPMSGVMIFGKESAGASTALDN 420
DB 497 NSNFTWGTASKYNLNGRESINPGTAMASHKDDKDFPMSGVMIFGKESAGASTALDN 556
QY 421 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWQDRDLYLQGP 480
DB 557 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWQDRDLYLQGP 616
```

```
QY 481 IWAKIPHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPPAPESATKFASTTQYSTG 540
DB 617 IWAKIPHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPPPTNSSAKFASFTQYSTG 676
QY 541 QVSVEIEMELQKENSCKRMNPEVOYTSNYSKANSANDFTVDNNGLYTERPIGTRILTRPL 599
DB 677 QVSVEIEMELQKENSCKRMNPEIQYTSNYSKANSVNDFTVDNNGVSEBRPIGTRILTRNL 735
```

RESULT 11

```
Q6JB21_9VIRU PRELIMINARY; PRT; 735 AA.
ID Q6JB21_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JB21;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Capsid protein VPI.
DE Name=cap;
GN Adeno-associated virus.
OS Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
CX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues."
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530628; AAS99270.1; -; Genomic_DNA.
DR SMR; Q6JB21; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81868 MW; 1654BD6287F5474 CRC64;
```

```
Query Match 86.7%; Score 2818.5; DB 2; Length 735;
Best Local Similarity 84.5%; Pred. No. 4.1e-166;
Matches 506; Conservative 40; Mismatches 52; Indels 1; Gaps 1;
```

```
QY 1 TAPGKKRPVEGSPQEPDSSSGIGKTGOQPAKRLNFGQTGDSSEVPDPQIGSEPPATPA 60
DB 138 TAPGKKRPVEHSPVEPDSSSGTGKAGQPARAKRLNFGQTGADSVDPDQIGSEPPAASG 197
QY 61 VGPPTMASGGGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTSRTMALPTYNHLY 120
DB 198 LGSTTMATGSGAPMADNNEGADGVGNASGNMHCDSQMLGDRVITTSRTMALPTYNHLY 257
QY 121 KOISSASTGASNDNHYFGYSTPMGYPDPNRFCHSPRDMQRLINNMGFRPKLNFKLF 180
DB 258 KOISSOS-GASNDNHYFGYSTPMGYPDPNRFCHSPRDMQRLINNMGFRPKLNFKLF 316
QY 181 NIQVEVTTNDGVTIANNLSTVQVFSDESEYQLPYVLGSAHQGLPEPPADVMIPOYG 240
DB 317 NIQVEVTTNDGVTIANNLSTVQVFSDESEYQLPYVLGSAHQGLPEPPADVMIPOYG 376
QY 241 YLTLLNGSAOAVGRSSFYCLEYFPSCMLRTGNFTFSYEEVPFHSSVYAHQSGLDRLNMP 300
DB 377 YLTLLNGSAOAVGRSSFYCLEYFPSCMLRTGNFTFSYEEVPFHSSVYAHQSGLDRLNMP 436
QY 301 LIDQVLYLNTQNSGSAQKDLFSRGSAPGMSVOPKJMLPGPCYRQOQSVSKTKTDNN 360
DB 437 LIDQVLYLNTQNSGSAQKDLFSRGSAPGMSVOPKJMLPGPCYRQOQSVSKTKTDNN 496
QY 361 NSNFTWGTASKYNLNGRESINPGTAMASHKDDKDFPMSGVMIFGKESAGASTALDN 420
DB 497 NSNFTWGTASKYNLNGRESINPGTAMASHKDDKDFPMSGVMIFGKESAGASTALDN 556
QY 421 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWQDRDLYLQGP 480
DB 557 VMTDEEIRKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWQDRDLYLQGP 616
```

QY 481 IWAKI PHTDGHFHPSPLMGFGSLKNPPQIILIKNTVPANPPAESATYFASFTIOYSTG 540
DB 617 IWAKI PHTDGHFHPSPLMGFGSLKNPPQIIMIKNTVPANPPPTNFSSAKFASFTIOYSTG 676
QY 541 QVSVLEIEMELOKENSKRNNPEIQTYSNYSKASANVDFTVNNGLYTEPRPIGRIYLRPL 599
DB 677 QVSVLEIEMELOKENSKRNNPEIQTYSNYSKASVNVDFVTJNGVSEPRPIGRIYLRNL 735

RESULT 12

Q6JBZ7_9VIRU PRELIMINARY; PRT: 735 AA.
ID Q6JBZ7_9VIRU
AC Q6JBZ7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X., Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530622; AAS9307.1; -; Genomic_DNA.
DR SMR; Q6JBZ7; 217-735.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A CRC64;

Query Match 86.7%; Score 2818.5; DB 2; Length 735;
Best Local Similarity 84.3%; Pred. No. 4.1e-186;
Matches 505; Conservative 41; Mismatches 52; Indels 1; Gaps 1;

QY 1 TAGGKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGQGTDSSEVPDPOGLSEPPATPA 60
DB 138 TAGGKRPVEHSPVEPDSSSGTGKAGQOPAKKRLNFGQGTDSSEVPDPOGLSEPPATPA 197
QY 61 VGETTMASSGGAPMADNNEGADGVGNASGNWCHDSITWLGDRVITTSRTMALPTYNHLY 120
DB 198 LGSITMATGSGAPMADNNEGADGVGNASGNWCHDSITWLGDRVITTSRTMALPTYNHLY 257
QY 121 KOISSASTGASNDNHFGYSTPWGYFDNRFCHFSRPMQORLINNKGFRPKRLNFKLF 180
DB 258 KOISSQS -GASNDNHFGYSTPWGYFDNRFCHFSRPMQORLINNKGFRPKRLNFKLF 316
QY 181 NIQVEKVTNDGVTIANNLSTVOVFSDEYQLPYVLSAHQGLCPPPADVFMIPQYG 240
DB 317 NIQVEKVTNDGVTIANNLSTVOVFTDSEYQLPYVLSAHQGLCPPPADVFMIPQYG 376
QY 241 YLTLLNGSQAVGSSSFYCLEYFPSPQMLRTGNNTFSTYEEVDFPHSSYAHQSGLDLRLMP 300
DB 377 YLTLLNGSQAVGSSSFYCLEYFPSPQMLRTGNNTFSTYEEVDFPHSSYAHQSGLDLRLMP 436
QY 301 LIDQVLYLNRTO -NOSGSAQNKDLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDN 360
DB 437 LIDQVLYLNRTOGTTTANLSTVOVFSDEYQLPYVLSAHQGLCPPPADVFMIPQYG 496
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDEKFFPMGSGVMI FGKESAGASNTALDN 420
DB 497 NSNFTWTGASKYNLNGRDSLVPNPGPAMASHKODEDEKFFPMGSGVMI FGKESAGASNTALDN 556
QY 421 NWITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWVQDRDYVLOG 480
DB 557 NWITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWVQDRDYVLOG 616

QY 481 IWAKI PHTDGHFHPSPLMGFGSLKNPPQIILIKNTVPANPPAESATYFASFTIOYSTG 540
DB 617 IWAKI PHTDGHFHPSPLMGFGSLKNPPQIIMIKNTVPANPPPTNFSSAKFASFTIOYSTG 676
QY 541 QVSVLEIEMELOKENSKRNNPEIQTYSNYSKASANVDFTVNNGLYTEPRPIGRIYLRPL 599
DB 677 QVSVLEIEMELOKENSKRNNPEIQTYSNYSKASVNVDFVTJNGVSEPRPIGRIYLRNL 735

RESULT 13

Q6S311_9VIRU PRELIMINARY; PRT: 736 AA.
ID Q6S311_9VIRU
AC Q6S311;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Capsid protein.
GN Adeno-associated virus 3.
OS Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=46350;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96266430; PubMed=8661429; DOI=10.1006/viro.1996.0367;
RA Muramatsu S., Mizukami H., Young N.S., Brown K.E.;
RT "Nucleotide sequencing and generation of an infectious clone of adeno-associated virus 3.";
RL Virology 221:208-217(1996).
DR EMBL; U48704; AAC55049.1; -; Genomic_DNA.
DR SMR; Q6S311; 217-736.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81660 MW; AF1EF47B5C67A10 CRC64;

Query Match 86.6%; Score 2815; DB 2; Length 736;
Best Local Similarity 85.2%; Pred. No. 7.1e-186;
Matches 511; Conservative 35; Mismatches 52; Indels 2; Gaps 2;

QY 1 TAGGKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGQGTDSSEVPDPOGLSEPPATPA 60
DB 138 TAGGKAADQSPQEPDSSSGVGSKOPAKKRLNFGQGTDSSEVPDPOGLSEPPATPA 197
QY 61 VGETTMASSGGAPMADNNEGADGVGNASGNWCHDSITWLGDRVITTSRTMALPTYNHLY 120
DB 198 LGSITMATGSGAPMADNNEGADGVGNASGNWCHDSITWLGDRVITTSRTMALPTYNHLY 257
QY 121 KOISSASTGASNDNHFGYSTPWGYFDNRFCHFSRPMQORLINNKGFRPKRLNFKLF 180
DB 258 KOISSQS -GASNDNHFGYSTPWGYFDNRFCHFSRPMQORLINNKGFRPKRLNFKLF 316
QY 181 NIQVEKVTNDGVTIANNLSTVOVFSDEYQLPYVLSAHQGLCPPPADVFMIPQYG 240
DB 317 NIQVEKVTNDGVTIANNLSTVOVFTDSEYQLPYVLSAHQGLCPPPADVFMIPQYG 376
QY 241 YLTLLNGSQAVGSSSFYCLEYFPSPQMLRTGNNTFSTYEEVDFPHSSYAHQSGLDLRLMP 300
DB 377 YLTLLNGSQAVGSSSFYCLEYFPSPQMLRTGNNTFSTYEEVDFPHSSYAHQSGLDLRLMP 436
QY 301 LIDQVLYLNRTO -NOSGSAQNKDLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDN 360
DB 437 LIDQVLYLNRTOGTTTANLSTVOVFSDEYQLPYVLSAHQGLCPPPADVFMIPQYG 496
QY 360 NSNFTWTGASKYNLNGRESIINPGTAMASHKODEDEKFFPMGSGVMI FGKESAGASNTALDN 419
DB 497 NSNFTWTGASKYNLNGRDSLVPNPGPAMASHKODEDEKFFPMGSGVMI FGKESAGASNTALDN 556
QY 420 NWITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWVQDRDYVLOG 479
DB 557 NWITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGCVHAMGALPGMWVQDRDYVLOG 616

QY 480 PIMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTLPVPANPAPESATKPFASFTIOYST 539
DB 617 PIMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTLPVPANPPTTFSAPKPFASFTIOYST 676
QY 540 QVSVEIEMELQKENS KRWNPPEVQYTSNYSKASANDFTVDNGLYTEPPPIGTRILYTRPL 599
DB 677 QVSVEIEMELQKENS KRWNPPEIQYTSNYSKASVNDFTVDNGLYSEPPPIGTRILYTRNL 736

RESULT 14

Q6JC17_VIRU
ID Q6JC17_VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JC17;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
tissues."
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530602; AAS99287.1; -; Genomic_DNA.
DR SMR; Q6JC17; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81887 MW; 709202P5EFFEB6EC CRC64;

Query Match 86.4%; Score 2808.5; DB 2; Length 735;
Best Local Similarity 84.3%; Pred. No. 2e-185;
Matches 505; Conservative 41; Mismatches 52; Indels 1; Gaps 1;
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DB 138 TAPGKKRPVEHSPVEPDSSSGTGKAGQPARKRLNFGQTGDSVDPDPLGEPAPASG 197
QY 61 VGPTTAGCGGAPMADNNEGADVGNASGNHCDSTWLGDRYITSTRMALPTYNHLY 120
DB 198 LGSTTMATGSGAPMADNNEGADVGNASGNHCDSTWLGDRYITSTRMALPTYNHLY 257
QY 121 KOISASTGASNDNHFGYSTPMGYFDNRFCHFSPPDMQRLINNNGFRPKRLNFKLF 180
DB 258 KOISGOS-GASNDNHFGYSTPMGYFDNRFCHFSPPDMQRLINNNGFRPKRLNFKLF 316
QY 181 NIQVEKVTNDGVTIANNLSTVQVPSDSEYQLPYLGSAHQGLPPPADVPMIPOYG 240
DB 317 NIQVEKVTNDGVTIANNLSTVQVPSDSEYQLPYLGSAHQGLPPPADVPMIPOYG 376
QY 241 YITLNGSAQVGRSSFFCLEYFPSCMLRTGNFTSYTTEBYRPHSSYAHSGSLRLNMP 300
DB 377 YITLNGSAQVGRSSFFCLEYFPSCMLRTGNFTSYTTEBYRPHSSYAHSGSLRLNMP 436
QY 301 LIDQVLYLNRQNGSAGNNDLFSRGS PAGMSVOPKMWLPGPCYRQQRVSKTKTDNN 360
DB 437 LIDQVLYLNRQNGSAGNNDLFSRGS PAGMSVOPKMWLPGPCYRQQRVSKTKTDNN 496
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FGKESAGASNTALDN 420
DB 497 NSNFTWTATATKYLHNRDGLVNGPAPAMASHKDEDEKFPMSGVMI FGKESAGASNTALDN 556
QY 421 VMTDEEIRKATNPVATERFGTVAVNFGSSSTDPATGVDYHANGALPGMWMDRDVYLQGP 480
DB 557 VMTDEEIRKATNPVATERFGTVAVNFGSSSTDPATGVDYHANGALPGMWMDRDVYLQGP 616

QY 481 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTLPVPANPAPESATKPFASFTIOYSTG 540
DB 617 IMAKIPHTDGHFHPSPLMGFGGLKNPPQILIKNTLPVPANPPTTFSAPKPFASFTIOYSTG 676
QY 541 QVSVEIEMELQKENS KRWNPPEVQYTSNYSKASANDFTVDNGLYTEPPPIGTRILYTRPL 599
DB 677 QVSVEIEMELQKENS KRWNPPEIQYTSNYSKASVNDFTVDNGLYSEPPPIGTRILYTRNL 735

RESULT 15

Q6JC38_VIRU
ID Q6JC38_VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JC38;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
tissues."
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530581; AAS99266.1; -; Genomic_DNA.
DR SMR; Q6JC38; 217-735.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81913 MW; 58131PDABE024251 CRC64;

Query Match 86.4%; Score 2807.5; DB 2; Length 735;
Best Local Similarity 84.1%; Pred. No. 2.4e-185;
Matches 504; Conservative 40; Mismatches 54; Indels 1; Gaps 1;
QY 1 TAPGKKRPVEGSPQEPDSSSGIGKTQQPARKRLNFGQTGDSBSVDPDPLGEPATPAA 60
DB 138 TAPGKKRPVEHSPVEPDSSSGTGKAGQPARKRLNFGQTGDSVDPDPLGEPAPASG 197
QY 61 VGPTTAGCGGAPMADNNEGADVGNASGNHCDSTWLGDRYITSTRMALPTYNHLY 120
DB 198 LGSTTMATGSGAPVADNNEGADVGNASGNHCDSTWLGDRYITSTRMALPTYNHLY 257
QY 121 KOISASTGASNDNHFGYSTPMGYFDNRFCHFSPPDMQRLINNNGFRPKRLNFKLF 180
DB 258 KOISGOS-GASNDNHFGYSTPMGYFDNRFCHFSPPDMQRLINNNGFRPKRLNFKLF 316
QY 181 NIQVEKVTNDGVTIANNLSTVQVPSDSEYQLPYLGSAHQGLPPPADVPMIPOYG 240
DB 317 NIQVEKVTNDGVTIANNLSTVQVPSDSEYQLPYLGSAHQGLPPPADVPMIPOYG 376
QY 241 YITLNGSAQVGRSSFFCLEYFPSCMLRTGNFTSYTTEBYRPHSSYAHSGSLRLNMP 300
DB 377 YITLNGSAQVGRSSFFCLEYFPSCMLRTGNFTSYTTEBYRPHSSYAHSGSLRLNMP 436
QY 301 LIDQVLYLNRQNGSAGNNDLFSRGS PAGMSVOPKMWLPGPCYRQQRVSKTKTDNN 360
DB 437 LIDQVLYLNRQNGSAGNNDLFSRGS PAGMSVOPKMWLPGPCYRQQRVSKTKTDNN 496
QY 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FGKESAGASNTALDN 420
DB 497 NSNFTWTATATKYLHNRDGLVNGPAPAMASHKDEDEKFPMSGVMI FGKESAGASNTALDN 556
QY 421 VMTDEEIRKATNPVATERFGTVAVNFGSSSTDPATGVDYHANGALPGMWMDRDVYLQGP 480
DB 557 VMTDEEIRKATNPVATERFGTVAVNFGSSSTDPATGVDYHANGALPGMWMDRDVYLQGP 616

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OM protein - protein search, using sw model

Run on: November 23, 2005, 17:26:29 ; Search time 27.2418 Seconds
(without alignment)
1817.892 Million cell updates/sec

Title: US-10-696-282-15

Perfect score: 3251
Sequence: 1 TAPGKKRPVEQSPQEPDSSS.....NNGLYTEPRPICTRYLTRPL 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seque, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5.COMB.pep: *
2: /cgn2_6/prodata/1/iaa/6.COMB.pep: *
3: /cgn2_6/prodata/1/iaa/H.COMB.pep: *
4: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep: *
5: /cgn2_6/prodata/1/iaa/RE.COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3251	100.0	599	2	US-09-807-802A-15
2	3251	100.0	736	2	US-09-807-802A-3
3	3251	100.0	736	2	US-09-807-802A-13
4	2906	89.4	534	2	US-09-807-802A-17
5	2764.5	85.0	735	2	US-09-321-589-1
6	2764.5	85.0	735	2	US-10-293-478-1
7	2764.5	85.0	735	2	US-10-038-972A-13
8	2759.5	84.9	539	2	US-10-038-972A-14
9	2481.5	76.3	533	2	US-10-038-972A-15
10	1830.5	56.3	598	2	US-09-532-594B-16
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12	1700.5	52.3	588	2	US-09-533-427-5
13	1700.5	52.3	724	2	US-09-533-427-4
14	1690.5	52.0	544	2	US-09-532-594B-18
15	1665	51.2	532	2	US-09-533-427-6
16	772	23.7	756	2	US-09-438-268-4
17	493	15.2	781	2	US-10-187-253E-27
18	486	14.9	554	2	US-10-187-253E-29
19	486	14.9	554	2	US-10-187-253E-35
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21	479.5	14.7	543	2	US-08-856-841-22
22	326	10.0	415	2	US-08-856-841-20
23	325	10.0	486	2	US-08-856-841-19
24	325	10.0	500	2	US-08-856-841-16
25	325	10.0	501	2	US-08-856-841-18
26	318	9.8	395	2	US-08-856-841-13
27	310	9.5	264	2	US-08-856-841-14

28	303	9.3	398	2	US-08-856-841-21	Sequence 21, App1
29	216.5	6.7	579	6	5223424-13	Patent No. 5223424
30	192	5.9	584	2	US-09-022-949-2	Sequence 2, App1
31	178.5	5.5	387	2	US-08-856-841-17	Sequence 17, App1
32	132.5	4.1	489	2	US-10-376-397B-4	Sequence 3855, Ap
33	119	3.7	1095	2	US-09-107-532A-3855	Sequence 4, App1
34	115	3.5	781	2	US-10-164-595-4	Sequence 4, App1
35	115	3.5	2283	2	US-10-172-502-4	Sequence 3027, A
36	115	3.5	2736	2	US-09-252-991A-10227	Sequence 27, App1
37	113.5	3.5	655	1	US-08-469-202-27	Sequence 34, App1
38	113.5	3.5	655	1	US-08-484-434C-34	Sequence 34, App1
39	113.5	3.5	655	2	US-09-384-361-34	Sequence 14, App1
40	112.5	3.5	3060	1	US-08-487-826B-14	Sequence 28, App1
41	111.5	3.4	551	2	US-09-248-796A-23413	Sequence 78, App1
42	110.5	3.4	624	2	US-08-947-965-78	Sequence 28, App1
43	110.5	3.4	655	1	US-08-469-202-28	Sequence 35, App1
44	110.5	3.4	655	1	US-08-484-434C-35	Sequence 35, App1
45	110.5	3.4	655	2	US-09-384-361-35	Sequence 35, App1

ALIGNMENTS

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RESULT 1
US-09-807-802A-15
Sequence 15, Application US/09807802A
Patent No. 6759237
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVN.031USA
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 599
TYPE: PRT
ORGANISM: AAV-1
US-09-807-802A-15
Query Match 100.0%; Score 3251; DB 2; Length 599;
Best Local Similarity 100.0%; Pred No. 1.1e-280; Indels 0; Gaps 0;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGTGDSSEVPDPPLGEPATPAA 60
1 TAPGKKRPVEQSPQEPDSSSGIGKTGQOPAKKRLNFGTGDSSEVPDPPLGEPATPAA 60
61 VEGTTMASGGGAPMADNNEGADGVGNASGNWCHDSITWLDGRTVITSTRTVALPTNNHLY 120
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181 NIQKKEVTINDGVTTIANNLITSTVQVFSSEYQLPVLSAHQGLPPPADVFMIPOYG 240
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241 YLTLLNGSQAVGSSSYCLFYPSSQMLRTGNNTFSTPBEPVPHSSYASOSLDRUMP 300
241 YLTLLNGSQAVGSSSYCLFYPSSQMLRTGNNTFSTPBEPVPHSSYASOSLDRUMP 300
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Db 421 VMTDEEIKATNPVATERFGTAVNFOSSSTDPAIDGVAMGALPGMWQDRDVTYLOGP 480
Qy 481 IMAKIPHTDGHFHSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTG 540
Db 481 IMAKIPHTDGHFHSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTG 540
Qy 541 QVSVEIEMELQENSKRMNPEVOYTSNYAKSANDVFTVDNNGLYTEBRPIGTRLYTRPL 599
Db 541 QVSVEIEMELQENSKRMNPEVOYTSNYAKSANDVFTVDNNGLYTEBRPIGTRLYTRPL 599

RESULT 2

US-09-807-802A-3
; Sequence 3, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPVN.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-3

Query Match 100.0%; Score 3251; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.5e-280;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAPGKKRPVEQSPQEPDSSSGIGKTGOQPAKKRLNFGQTDSESVPPDPLGEPATPAA 60
Db 138 TAPGKKRPVEQSPQEPDSSSGIGKTGOQPAKKRLNFGQTDSESVPPDPLGEPATPAA 197
Qy 61 VGPPTMASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITSTRTMAIPTYNHLY 120
Db 198 VGPPTMASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITSTRTMAIPTYNHLY 257
Qy 121 KOISSASTASNDNHFGYSTPMGWYFDENRFCHSPDQRLINNMMGFRPKLNFLF 180
Db 258 KOISSASTASNDNHFGYSTPMGWYFDENRFCHSPDQRLINNMMGFRPKLNFLF 317
Qy 181 NIQVEVTNDGVTITANNLSTVOVFSDSSEYOLPYVLGSAHQGLPPFPADVMIPOYG 240
Db 318 NIQVEVTNDGVTITANNLSTVOVFSDSSEYOLPYVLGSAHQGLPPFPADVMIPOYG 377
Qy 241 YLTLLNGSOAVGRSFFCYCLEYFPQMLRTGNFTFSTFEEVPHSSYAHQSOLDRLMNP 300
Db 378 YLTLLNGSOAVGRSFFCYCLEYFPQMLRTGNFTFSTFEEVPHSSYAHQSOLDRLMNP 437
Qy 301 LIDQYLYLNTQNGSGAQNKDILFSRGSAPAGMSVQPKNMLPGPCYRQGRVSKTKTDNN 360
Db 438 LIDQYLYLNTQNGSGAQNKDILFSRGSAPAGMSVQPKNMLPGPCYRQGRVSKTKTDNN 497
Qy 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASNTALDN 420

Db 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASNTALDN 557
Qy 421 VMTDEEIKATNPVATERFGTAVNFOSSSTDPAIDGVAMGALPGMWQDRDVTYLOGP 480
Db 558 VMTDEEIKATNPVATERFGTAVNFOSSSTDPAIDGVAMGALPGMWQDRDVTYLOGP 617
Qy 481 IMAKIPHTDGHFHSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTG 540
Db 618 IMAKIPHTDGHFHSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTG 677
Qy 541 QVSVEIEMELQENSKRMNPEVOYTSNYAKSANDVFTVDNNGLYTEBRPIGTRLYTRPL 599
Db 678 QVSVEIEMELQENSKRMNPEVOYTSNYAKSANDVFTVDNNGLYTEBRPIGTRLYTRPL 736

RESULT 3

US-09-807-802A-13
; Sequence 13, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPVN.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-13

Query Match 100.0%; Score 3251; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.5e-280;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAPGKKRPVEQSPQEPDSSSGIGKTGOQPAKKRLNFGQTDSESVPPDPLGEPATPAA 60
Db 138 TAPGKKRPVEQSPQEPDSSSGIGKTGOQPAKKRLNFGQTDSESVPPDPLGEPATPAA 197
Qy 61 VGPPTMASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITSTRTMAIPTYNHLY 120
Db 198 VGPPTMASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITSTRTMAIPTYNHLY 257
Qy 121 KOISSASTASNDNHFGYSTPMGWYFDENRFCHSPDQRLINNMMGFRPKLNFLF 180
Db 258 KOISSASTASNDNHFGYSTPMGWYFDENRFCHSPDQRLINNMMGFRPKLNFLF 317
Qy 181 NIQVEVTNDGVTITANNLSTVOVFSDSSEYOLPYVLGSAHQGLPPFPADVMIPOYG 240
Db 318 NIQVEVTNDGVTITANNLSTVOVFSDSSEYOLPYVLGSAHQGLPPFPADVMIPOYG 377
Qy 241 YLTLLNGSOAVGRSFFCYCLEYFPQMLRTGNFTFSTFEEVPHSSYAHQSOLDRLMNP 300
Db 378 YLTLLNGSOAVGRSFFCYCLEYFPQMLRTGNFTFSTFEEVPHSSYAHQSOLDRLMNP 437
Qy 301 LIDQYLYLNTQNGSGAQNKDILFSRGSAPAGMSVQPKNMLPGPCYRQGRVSKTKTDNN 360
Db 438 LIDQYLYLNTQNGSGAQNKDILFSRGSAPAGMSVQPKNMLPGPCYRQGRVSKTKTDNN 497
Qy 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASNTALDN 420
Db 498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASNTALDN 557
Qy 421 VMTDEEIKATNPVATERFGTAVNFOSSSTDPAIDGVAMGALPGMWQDRDVTYLOGP 480

Db 558 VMTTDEEIKATNPVATERFGTVAANFGSSSTDPATGDVHAGALPGMWQODRDVYLQGP 617

Qy 481 IWAKIPHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 540

Db 618 IWAKIPHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 677

Qy 541 QVSVEIEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 599

Db 678 QVSVEIEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 736

RESULT 4

US-09-807-802A-17

Sequence 17, Application US/09807802A

Patent No. 6759237

GENERAL INFORMATION:

APPLICANT: Wilson, James M.

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,

TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVN.031USA

CURRENT APPLICATION NUMBER: US/09/807,802A

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patent in version 3.1

SEQ ID NO 17

LENGTH: 534

TYPE: PRT

ORGANISM: AAV-1

US-09-807-802A-17

Query Match 89.4%; Score 2906; DB 2; Length 534;

Best Local Similarity 100.0%; Pred. No. 5e-250;

Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 MASGGGAPMADNNEGADGVNAGNWHCDSTWLGDRVITTSRTMALPTYNNHLYKQISS 125

Db 1 MASGGGAPMADNNEGADGVNAGNWHCDSTWLGDRVITTSRTMALPTYNNHLYKQISS 60

Qy 126 ASTGASNDNHFGYSTPFGYFDFNRFCHFSPRDMQRLINNMGFRKRLNFKLFNIQVK 185

Db 61 ASTGASNDNHFGYSTPFGYFDFNRFCHFSPRDMQRLINNMGFRKRLNFKLFNIQVK 120

Qy 186 EVTTNDGVTTIANNLSTVOVPSDSEYQLPYVLGSAHQGLPPRPADVPMIPOYGYLTN 245

Db 121 EVTTNDGVTTIANNLSTVOVPSDSEYQLPYVLGSAHQGLPPRPADVPMIPOYGYLTN 180

Qy 246 NSGOAVRRSFCLEYPFSQMLRTGNFTFSYTFEEVPHSSVYAHQSGLDRMLNP 305

Db 181 NSGOAVRRSFCLEYPFSQMLRTGNFTFSYTFEEVPHSSVYAHQSGLDRMLNP 240

Qy 306 LYYLNRFGONSGAQNKDLFSRGS PAMGSYQPKWLPGPCYRQQRVSKTKTDNNNSFT 365

Db 241 LYYLNRFGONSGAQNKDLFSRGS PAMGSYQPKWLPGPCYRQQRVSKTKTDNNNSFT 300

Qy 366 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGVMTFGKESAGASNTALDNMTD 425

Db 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGVMTFGKESAGASNTALDNMTD 360

Qy 426 EEEKATNPVATERFGTVAANFGSSSTDPATGDVHAGALPGMWQODRDVYLQGP 485

Db 361 EEEKATNPVATERFGTVAANFGSSSTDPATGDVHAGALPGMWQODRDVYLQGP 420

Qy 486 PHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 545

Db 421 PHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 480

Qy 546 IEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 599

Db 481 IEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 534

RESULT 5

US-09-321-589-1

Sequence 1, Application US/09321589

Patent No. 6498244

GENERAL INFORMATION:

APPLICANT: PATEL, SALLI D.

APPLICANT: MCARTHUR, JAMES G.

TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS

FILE REFERENCE: 39672

CURRENT APPLICATION NUMBER: US/09/321,589

PRIOR FILING DATE: 1999-05-28

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 1

LENGTH: 735

TYPE: PRT

ORGANISM: Adeno-associated virus

US-09-321-589-1

Query Match 85.0%; Score 2764.5; DB 2; Length 735;

Best Local Similarity 82.8%; Pred. No. 3.3e-237;

Matches 496; Conservative 43; Mismatches 59; Indels 1; Gaps 1;

Qy 1 TAPGKKRPVEQSPQEPDSSSGIGTGGQQAQKRLNFGQGDSESVDDPQPLGEPATPPA 60

Db 138 TAPGKKRPVEHSPVEPDSSTSGTGAKGQOPARRLNFGQGDSDVBDPQPLGQPPAPFG 197

Qy 61 VEPPTMASGGGAPMADNNEGADGVNAGNWHCDSTWLGDRVITTSRTMALPTYNNHLY 120

Db 198 LGTNTMATSGAPMANNNEGADGVNAGNWHCDSTWLGDRVITTSRTMALPTYNNHLY 257

Qy 121 KQISSASTGASNDNHFGYSTPFGYFDFNRFCHFSPRDMQRLINNMGFRKRLNFKLF 180

Db 258 KQISSGS-GASNDNHFGYSTPFGYFDFNRFCHFSPRDMQRLINNMGFRKRLNFKLF 316

Qy 181 NIQKEVTTNDGVTTIANNLSTVOVPSDSEYQLPYVLGSAHQGLPPRPADVPMIPOYGY 240

Db 317 NIQKEVTTNDGVTTIANNLSTVOVPSDSEYQLPYVLGSAHQGLPPRPADVPMIPOYGY 376

Qy 241 YLTNNGSOAVGSSFCLEYPFSQMLRTGNFTFSYTFEEVPHSSVYAHQSGLDRMLNP 300

Db 377 YLTNNGSOAVGSSFCLEYPFSQMLRTGNFTFSYTFEEVPHSSVYAHQSGLDRMLNP 436

Qy 301 LIDQVLYLNRFGONSGAQNKDLFSRGS PAMGSYQPKWLPGPCYRQQRVSKTKTDNN 360

Db 437 LIDQVLYLNRFGONSGAQNKDLFSRGS PAMGSYQPKWLPGPCYRQQRVSKTKTDNN 496

Qy 361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGVMTFGKESAGASNTALDN 420

Db 497 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGVMTFGKESAGASNTALDN 556

Qy 421 VMTTDEEIKATNPVATERFGTVAANFGSSSTDPATGDVHAGALPGMWQODRDVYLQGP 480

Db 557 VMTTDEEIKATNPVATERFGTVAANFGSSSTDPATGDVHAGALPGMWQODRDVYLQGP 616

Qy 481 IWAKIPHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 540

Db 617 IWAKIPHTDGHFHPSPMLMGFGFKNPPQILIKNTVPANPAPFASATKFASTTQYSTG 676

Qy 541 QVSVEIEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 599

Db 677 QVSVEIEMELOKENSKRMPNPEVOYTSNYAKSANVDTVDNNGLYTEPRPIGTRYLRLPL 735

RESULT 6

US-10-293-478-1

Sequence 1, Application US/10293478

Patent No. 6733757

GENERAL INFORMATION:

APPLICANT: PATEL, SALLI D.

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; APPLICANT: MCARTHUR, JAMES G.
; TITLE OF INVENTION: ADEMO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/10/293,478
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/321,589
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Adeno-associated virus
US-10-293-478-1

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Query Match      85.0%; Score 2764.5; DB 2; Length 735;
Best Local Similarity 82.8%; Pred. No. 3.3e-237;
Matches 496; Conservative 43; Mismatches 59; Indels 1; Gaps 1;

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QY 1 TAPGKRPVEOSPOEPPSSSGIGTKGQOPAKKRLNFGQTGDSSEVPDPQPLGEPPATPAA 60
DB 138 TAPGKRPVEHSPVEPDSSSGTGKAGQOPAKKRLNFGQTGDSVPDPQPLGPPAASG 197
QY 61 VGPPTMASGGA PMADNNEGADGVGNASGNMHCSTWLGDRVITSTRTALPTYNNHLY 120
DB 198 LGTMTATGSGA PMADNNEGADGVGNASGNMHCSTWMDRVITSTRTALPTYNNHLY 257
QY 121 KOISSASTGASNDNHYFGYSTPMGYFDPNRFCHFSRDMQRLINNMMGFPRKRLNFKLF 180
DB 258 KOISSQS-GASNDNHYFGYSTPMGYFDPNRFCHFSRDMQRLINNMMGFPRKRLNFKLF 316
QY 181 NIQVEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPFPADVPMIQYG 240
DB 317 NIQVEVTTNDGVTTIANNLSTVQVFTDSEYQLPYVLGSAHQCLPPFPADVPMIQYG 376
QY 241 YLTNNNGSQA VGRSSFYCLEYFPSPQMLRTGNNFTFSYTEEVPFHSSYAHQSGLDRLMNP 300
DB 377 YLTNNNGSQA VGRSSFYCLEYFPSPQMLRTGNNFTFSYTEEVPFHSSYAHQSGLDRLMNP 436
QY 301 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 360
DB 437 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 496
QY 437 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 496
DB 361 NSNFTWTSKYNLNGRESIIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDN 420
QY 497 NSEYSGATGATKYHLNGRDSLVPNGPAMASHKDEDEKFFPMGCVMI FGKESAGASTALDN 556
DB 421 VMTDEBEIKATNPVATERFGTVAVNFGSSSTDPAATGVHAMGALPGMWODRDVYLQGP 480
QY 557 VMTDEBEIKATNPVATERFGTVAVNFGSSSTDPAATGVHAMGALPGMWODRDVYLQGP 616
DB 481 IMAKIPHTDGHFHSPLMGSGFGLKNPPOILLIKNTPPANPAEFSATKFAFTTOYSTG 540
QY 617 IMAKIPHTDGHFHSPLMGSGFGLKNPPOILLIKNTPPANPAEFSATKFAFTTOYSTG 676
DB 541 QVSVEIEMELQKENS KRNMP EIVQYTSNYSKASANDFTVDNGLYTEPRPIGTRILTRPL 599
QY 677 QVSVEIEMELQKENS KRNMP EIVQYTSNYSKASANDFTVDNGLYTEPRPIGTRILTRNL 735

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RESULT 7
US-10-038-972A-13
; Sequence 13, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 735
; TYPE: PRT
; ORGANISM: adeno-associated virus 2 VP1 capsid protien
US-10-038-972A-13

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Query Match      85.0%; Score 2764.5; DB 2; Length 735;
Best Local Similarity 82.8%; Pred. No. 3.3e-237;
Matches 496; Conservative 43; Mismatches 59; Indels 1; Gaps 1;

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QY 1 TAPGKRPVEOSPOEPPSSSGIGTKGQOPAKKRLNFGQTGDSSEVPDPQPLGEPPATPAA 60
DB 138 TAPGKRPVEHSPVEPDSSSGTGKAGQOPAKKRLNFGQTGDSVPDPQPLGPPAASG 197
QY 61 VGPPTMASGGA PMADNNEGADGVGNASGNMHCSTWLGDRVITSTRTALPTYNNHLY 120
DB 198 LGTMTATGSGA PMADNNEGADGVGNASGNMHCSTWMDRVITSTRTALPTYNNHLY 257
QY 121 KOISSASTGASNDNHYFGYSTPMGYFDPNRFCHFSRDMQRLINNMMGFPRKRLNFKLF 180
DB 258 KOISSQS-GASNDNHYFGYSTPMGYFDPNRFCHFSRDMQRLINNMMGFPRKRLNFKLF 316
QY 181 NIQVEVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPFPADVPMIQYG 240
DB 317 NIQVEVTTNDGVTTIANNLSTVQVFTDSEYQLPYVLGSAHQCLPPFPADVPMIQYG 376
QY 241 YLTNNNGSQA VGRSSFYCLEYFPSPQMLRTGNNFTFSYTEEVPFHSSYAHQSGLDRLMNP 300
DB 377 YLTNNNGSQA VGRSSFYCLEYFPSPQMLRTGNNFTFSYTEEVPFHSSYAHQSGLDRLMNP 436
QY 301 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 360
DB 437 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 496
QY 437 LIDQVLYLNTQONQSGAONKDLFSGSPAGMSVOPKMLPGCYRQQRVSKTKTDNN 496
DB 361 NSNFTWTSKYNLNGRESIIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDN 420
QY 497 NSEYSGATGATKYHLNGRDSLVPNGPAMASHKDEDEKFFPMGCVMI FGKESAGASTALDN 556
DB 421 VMTDEBEIKATNPVATERFGTVAVNFGSSSTDPAATGVHAMGALPGMWODRDVYLQGP 480
QY 557 VMTDEBEIKATNPVATERFGTVAVNFGSSSTDPAATGVHAMGALPGMWODRDVYLQGP 616
DB 481 IMAKIPHTDGHFHSPLMGSGFGLKNPPOILLIKNTPPANPAEFSATKFAFTTOYSTG 540
QY 617 IMAKIPHTDGHFHSPLMGSGFGLKNPPOILLIKNTPPANPAEFSATKFAFTTOYSTG 676
DB 541 QVSVEIEMELQKENS KRNMP EIVQYTSNYSKASANDFTVDNGLYTEPRPIGTRILTRPL 599
QY 677 QVSVEIEMELQKENS KRNMP EIVQYTSNYSKASANDFTVDNGLYTEPRPIGTRILTRNL 735

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RESULT 8
US-10-038-972A-14
; Sequence 14, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 598
; TYPE: PRT
; ORGANISM: adeno-associated virus 2 VP2 capsid protien
US-10-038-972A-14

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Query Match      84.9%; Score 2759.5; DB 2; Length 598;

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	Best Local Similarity	82.8%;	Pred. No. 6.6e-237;	
	Matches	495;	Conservative	43; Mismatches 59; Indels 1; Gaps 1
Qy	2	APGKKRPVEQSPQEPDSSSGIGTKTQQQAPAKKRLNFGQIGDSSSVDPDPLGPPATPAAV	61	
Db	2	APGKKRPVEHSPVEPDSSSGTGKAGQAPARKRLNFGQTGDADSVDPDPLGPPAPASGL	61	
Qy	62	GPTMASGGGAPMADNMGADGVGNASGMWCHCDSTWMLGDRVITTSRTMALPTYNNHLTK	121	
Db	62	GTNTMATSGAPMANNMGADGVGNSSGMWCHCDSTWMLGDRVITTSRTMALPTYNNHLTK	121	
Qy	122	QISSASTASNDNHHFGYSTPMGCFYDFENRHHCHFSFPRDQRLINNMGPRPKRLNFKLFN	181	
Db	122	QISSOS-CASNDNHHFGYSTPMGCFYDFENRHHCHFSFPRDQRLINNMGPRPKRLNFKLFN	180	
Qy	182	IQVKEVTNDGVTTIANMLTSTVQVYFSDSEYQLPYVLGSAHQGCLPPPADVPMIPIQCY	241	
Db	181	IQVKEVTQNDGTTIANMLTSTVQVFTDSEYQLPYVLGSAHQGCLPPPADVPMVPOICY	240	
Qy	242	LTIANNGSAVGNSSSYCLEFPPSQMLRTGNNNTFTSTFEVPPHSSYAHSSQSLDRMLNPL	301	
Db	241	LTIANNGSAVGNSSSYCLEFPPSQMLRTGNNNTFTSTFEVPPHSSYAHSSQSLDRMLNPL	300	
Qy	302	IDQVLYYLNRTQNOGSAQNKOLLFSRGSFAGMSVQPKWMLGPCCYRQGRVSKTKTDNNN	361	
Db	301	IDQVLYYLSKRTTPEGTTTQSKLQFSQAGASDTRDQSRMLWLEQPCYRQGRVSKTSADNN	360	
Qy	362	SNFTWTGASKYNLNGRESIINPGTAMASHKDEDKFFPMGMYMFGKESAGASNTALDNV	421	
Db	361	SESVTGTGATKHYLNGRDSLIVNPGPAMASHKDEBEKFFPQGVILFGKQSEKTNVDIERKV	420	
Qy	422	MITDEBEIKNPVATERFGYVAVNFQSSSTDPATGDVYAMGALPBMWQDRVYLQGP	481	
Db	421	MITDEEBIRTTNPVATEQYGVSTYMLQRNROAATADVNTQGLPBMWQDRVYLQGP	480	
Qy	482	WAKIHTTGHFHPSPLMGEGFKNPPOLIKNTPPANPAPAFSATKTFASFTQYSTGQ	541	
Db	481	WAKIPTTDSHFHPSPLMGEGFKLHPPOLIKNTPIPANPSTTFSAKAKASFTQYSTGQ	540	
Qy	542	VSEVEIEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNNGLYTEBPIGTRYLTPPL	599	
Db	541	VSEVEIEMELQKNSKRMNPEIQTTSYNNKSVANDFTVDNNGVYSBRPIGTRYLTPPL	598	
RESULT 9				
US-10-038-972A-15				
; Sequence 15, Application US/10038972A				
; Patent No. 6962815				
; GENERAL INFORMATION:				
; APPLICANT: J. Bartlett				
; TITLE OF INVENTION: AAV VECTORS AND METHODS				
; FILE REFERENCE: 28335/36996US				
; CURRENT APPLICATION NUMBER: US/10/038, 972A				
; CURRENT FILING DATE: 2002-01-04				
; PRIOR APPLICATION NUMBER: US 60/260,124				
; PRIOR FILING DATE: 2001-01-05				
; NUMBER OF SEQ ID NOS: 18				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 15				
; LENGTH: 533				
; TYPE: PRT				
; ORGANISM: adeno-associated virus 2 VP3 capsid protien				
US-10-038-972A-15				
Query Match				
Best Local Similarity 83.3%; Pred. No 3.2e-212;				
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1				
Qy	66	MASGGAPMADNMGADGVGNASGMWCHCDSTWMLGDRVITTSRTMALPTYNNHLKYQISS	125	
Db	1	MATGSGAPMADNMGADGVGNSSGMWCHCDSTWMLGDRVITTSRTMALPTYNNHLKYQISS	60	
Qy	126	ASTGASNDNHHFGYSTPMGCFYDFENRHHCHFSFPRDQRLINNMGPRPKRLNFKLFN	185	

[illegible]

QY	122	QISSATGASNNHHVGYSTPMGYEDPNRFFCHSPRMOQLINNMGFPKLIENFLN	181
Db	113	EISGSGVSDSNANAIFGYSTPMGYEDPNRFFSHSPRMOQLINNMGFPKLIENFLN	172
QY	182	IQVKEVTTDGVTTIANMLTSTVOVFSDBEYQPYVLGSAHQGLPPPADVFNIPDGY	241
Db	173	IQVKEVTTDGVTTIANMLTSTVOVFTDDYQLPVVGNGTEGCLPAFPQVFTLPOGY	232
QY	242	LITLN-NSQOAVGRSSFYCLEYFPESQMLRTGNFTFESTEEVFPFHSYAHSGSLRLM	299
Db	233	ATLNRDNTENPTERSSEFPCLEYFPESKMLRTGNFNEFTTNFEEVFPFHSFAPSOULFRLAN	292
QY	300	ELIDVLYLINTQNGSGSAONKDLLFSKSGPAGSVP-RKNWPGCEYRQORVSKXTD	358
Db	293	PLVDQYLYRFVSTNNNGVQFPKNL-----AGRYANTYKMPGPMGRKQGNMLGSGV	345
QY	359	NNNSNFTWTGASKYNNINGRESEIINPECTAMASHKODEDKFPMSGVMIFGKESAGASNTAL	418
Db	346	NRASVSASFATINRMELEGASYOVPPOPNOMTNNLGSTYVALBMTMLFNQSPANPGTAT	405
QY	419	---DNWMTDEBEIKATNPVATEREFGYAVNFQSSSTDPATGDVHANGALPGMWQDRDY	475
Db	406	YLEGNMLTISESTQVNRVAVNVGQMATNNQSSSTAPATGYTALDEIVPGSYMMRBDV	465
QY	476	YLOGPIWAKIPHTDGHFHPSPLMGGGGLKNPPQILLIKTTPVNPANPRAEPATFPAFIT	535
Db	466	YLOGPIWAKIPETGALFHPSPAMGGGLKHPMMMLIKTTPVPGI-ITFSFDDVSSFIT	524
QY	536	OYSTQGVSVIEIWELOKENSKRNNPVOUTSYTAAVSANVDFVTDNNGLYTEPRPIGRYL	593
Db	525	OYSTQGVYTEMELKENSKRNNPEIQTNNYNDPQFVDPAPODSTGBYRTTRPIGRYL	584
QY	596	TRPL 599	
Db	585	TRPL 588	

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RESULT 13
US-09-533-427-4
: Sequence 4, Application US/09533427
: Patent No. 6855314
: GENERAL INFORMATION:
: APPLICANT: Klotin, John
: APPLICANT: Klotin, Robert M.
: APPLICANT: Saefer, Brian
: APPLICANT: Davidson, Elizabeth
: APPLICANT: Zahner, Joseph
: TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRAIN CELLS AND LONG CELLS
: FILE REFERENCE: 14014.032302
: CURRENT APPLICATION NUMBER: US/09/533.427
: CURRENT FILING DATE: 2000-03-22
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 724
: TYPE: PRT
: ORGANISM: Artificial Sequence
FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: /No. 6855314e =
: OTHER INFORMATION: Synthetic construct
US-09-533-427-4

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Query Match 152.3%; Score 1700.5; DB 2; Length 724;
Best Local Similarity 55.0%; Pred. No. 1.9e-142;
Matches 332; Conservative 64; Mismatches 173; Indels 35; Gaps 7;

QY 3 PCKRKPVGQSPOEPPSSGIGKGTGGQPAKKRLNFGQDSSEVPPQPLGEPPTPA-AV 61
Db 149 PCKRKARTEBDSKPTSS-----DAEGPSSGSQLQIPAPQASL 188

QY 62 GFTTASGGGAPMADNNEGADGVNAGSNWCHDSTWGLDGVYITTSRTWALPTYNNHLYK 121
Db 189 GADTYSAGGGGGLGNNOGADGVNAGSNWCHDSTWMDGDRVYTKSTRTWLPSTYNNHLYR 248

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QY	122	QISSASGASNDNYHFGSTPMGCFEDFNRFHCFHSEPRDMOQLINNNMGRPRKLNKFN	181
Db	249	EIKSGSDGSIANNAYFGISTPMGTFYDFRFRHSHMSPRDMOQLINNNMGRPRSLRKIN	308
QY	182	IQVEKVTINDGVTTIANNLSTVOYFSDSEYQLPVYLGSAMHGCLPRPPADVPMIDQY	241
Db	309	IQVEEVYQDSTTTIANNLSTVOYFTDDYQLPVYVNGSTEGCLPAPFPQVFTLEPQY	368
QY	242	LTIN-NGSQAVGRSSPYCLEYFPBSQMLRTGNFFSTFEENVPPHSSYAHOSQLDRLN	299
Db	369	ATLRNDTENPTEBSSFPCELYFPBSKMLRTGNFFFTYFBEVPPHSSAPBSQNLKFLN	428
QY	300	PLIDYOYLTLNKRQONQSSAQNKDILFGRSGPAGMSVQP-KMWLGPCCVROORVSKTKD	358
Db	429	PLVQOYLFRVSTNNGTGVOYFQFKNL-----AGRYANTYKMPFQPMGRTOGMNIGSV	481
QY	359	NNNSFTWTGASKYVLANGRESIINGTAMASHKDEDEKFFPMSGVMIFCKESAGASNTAL	418
Db	482	NRASVASPATNNRRELBGASQVPPQPMGMTNNLOGSNITYALENTMIFRISQAPNPGTTAT	541
QY	419	--DNVMITDEEBEIKATNPVATERPFTVAVNFQSSSTDPATGDVHAMGALPGMWTODRDV	475
Db	542	YLEGMMLTSSSETPQVNRVAVNVGQMAVNNQSSITABATGYNLQEIIVPGSVMMERDV	601
QY	476	YLOGPIWAKIPHTDGHFHPSPLMGSGFLKNPPOLLIKTVPANPAPAFSATKFSFT	535
Db	602	YLOGPIWAKIPETGAHFHPSPAMGSGFLKHPPMMLIKTVPBGN-ITFSQVPPVSSFT	660
QY	536	QYSTQGVSELEFMELOKENSKRMPNEVOYTSNYAASANDPFTVDDNGLTBPPICTRYL	595
Db	661	QYSTQGVSELEFMELOKENSKRMPNEVOYTSNYAASANDPFTVDDNGLTBPPICTRYL	720
QY	596	TRPL 599	
Db	721	TRPL 724	

```

RESULT 14
US-09-532-594B-18
; Sequence 18, Application US/09532594B
; Patent No. 6468524
; GENERAL INFORMATION:
; APPLICANT: Chorini, John A.
; APPLICANT: Korin, Robert M.
; APPLICANT: Saefer, Brian
; APPLICANT: Davidson, Beverly
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; FILE REFERENCE: 14014.0252U2
; CURRENT APPLICATION NUMBER: US/09/532,594B
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e =
; OTHER INFORMATION: synthetic construct
; NAME/KEY: misc feature
; OTHER INFORMATION: AAV4 capsid protein VP3
US-09-532-594B-18

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[illegible]

```

Db      67  ---SIQSTHTYNGFSPWCGYFDENRPHCHSPSPDWRLLNNNMGMKPKAMRYKIFNIQYKE 123
Qy      187 VTTNDGVTTIANNLSTVQVFSDBEYQLPYVLGSAHOGCLPPFPADVFMIPQYGT---LT 243
Db      124 VTTSGEFTVANNLSTVQIFPADSSYELPYVMDAQBGSLPPFPADVFMVPOYGCGLVT 183
Qy      244 LUNGSAVGRSSFYCLEYFPSPOMLRTGNNTFTSYFEFVPPHSSVAHSOSLDRLMNPILD 303
Db      184 GNTSQOQTDNRNAFYCLEYFPSPOMLRTGNNTFTSYFEFVPPHSSVAHSOSLDRLMNPILD 243
Qy      304 QYLYLNRTON---QSGSAQNKDILLFSGSPAGMSVOPKMWLPGPCYRQORVSKTKTDN 359
Db      244 QYLMWLGSTTTGTTLNAGATTN---FTKLRPTNSNFKMWLPGPSIKQOGFSKTA--N 298
Qy      360 NNSNTWTGAS---KY---NLNGRESIIINPGTAMASHKODEDKFFPMGVMIPKESAG 412
Db      299 QNYKIPATGSDSLIYETHSTLDGWSALTPGPAPATAGPADSK--FNSNOLIFAGPKONG 357
Qy      413 ASNTALDNVMTDEBEIKATNPATERFGTVAVNFQSSSTDPATGDVHAMGALPGMWQD 472
Db      358 NTAATPGULIFTESEELATNATDTDMGNLPGGQSSNLPFTVRLTALGAVPGMWQN 417
Qy      473 RDVYLQGPIMAKIPHTDGHFHPSPLMGGFGLKNPPQILIKNTVPANPAPAFSATKPEAS 532
Db      418 RDIYQGPIMAKIPHTDGHFHPSPLMGGFGLKNPPQILIKNTVPANPAPAFSSTPVNS 477
Qy      533 FITQSTQGVSEIEMWLOKENSCKMNPVQYTSNYAKSANDFTVDNNGLYTEBRPIGT 592
Db      478 FITQSTQGVSEIEMWLOKENSCKMNPVQYTSNYAKSANDFTVDNNGLYTEBRPIGT 537
Qy      593 RYLTRPL 599
Db      538 RYLTRPL 544

```

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RESULT 15
US-09-533-427-6
/ Sequence 6, Application US/09533427
/ Patent No. 6855314
/ GENERAL INFORMATION:
/ APPLICANT: Chlorini, John
/ APPLICANT: Kolin, Robert M.
/ APPLICANT: Safer, Brian
/ APPLICANT: Davidson, Elizabeth
/ APPLICANT: Zahner, Joseph
/ TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
/ FILE REFERENCE: 14014.032302
/ CURRENT APPLICATION NUMBER: US/09/533,427
/ CURRENT FILING DATE: 2000-03-22
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 532
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e =
/ OTHER INFORMATION: synthetic construct
US-09-533-427-6

```

```

Query Match      51.2%; Score 1665; DB 2; Length 532;
Best Local Similarity 58.9%; Pred. No. 17e-139;
Matches 318; Conservative 54; Mismatches 154; Indels 14; Gaps 5;

```

```

Qy      66 MASGGAPVADNNEGADGVGNAAGNHCDSITWLGDRVITTSRTIALPTNNHLYKQISS 125
Db      1  MASGGGGPLGDNNQAGDGVGNAAGNHCDSITWLGDRVITTSRTIALPTNNHLYKQISS 60
Qy      126 ASTGASNDNHHYGYSTPMWGYFDENRPHCHSPSPDWRLLNNNMGPRPKLNFKLNIQYK 185
Db      61 GSVDSGNANAYFGYSTPMWGYFDENRPHCHSPSPDWRLLNNNMGPRPKLNFKLNIQYK 120

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Qy      186 EVTTNDGVTTIANNLSTVQVFSDBEYQLPYVLGSAHOGCLPPFPADVFMIPQYGLTLN 245
Db      121 EVTVQDSTTTIIANNLSTVQVFTDDYQLPYVNGNGBGCLPAPPGVFTLLPQYGVATLN 180
Qy      246 --NSQA VGRSSFYCLEYFPSPOMLRTGNNTFTSYFEFVPPHSSVAHSOSLDRLMNPILD 303
Db      181 RDNTENPTERRSSFPCLYFPSPOMLRTGNNTFTSYFEFVPPHSSVAHSOSLDRLMNPILD 240
Qy      304 QYLYLNRTONQSGSAQNKDILLFSGSPAGMSVOP--KNWLPGPCYRQORVSKTKTDNNS 362
Db      241 QYLYRFTVSTNTGTVQVFNKNL-----AGRYANTYKMFPGMGRTOGMVLSGVNRAS 293
Qy      363 NFWTGA SKYVNLNGRESIIINPGTAMASHKODEDKFFPMGVMIPKESAGASNTAL---D 419
Db      294 VSAFATINRMELBEGASVQVPPQPMGNTNNGSNTALNTMINSQPANGTATYLEG 353
Qy      420 NMVITDEBEIKATNPATERFGTVAVNFQSSSTDPATGDVHAMGALPGMWQDDVYLOG 479
Db      354 NMLITSESETOPVNRVAVNVGOMATNQSSTTAPATGYTLQBIVPQSVMEKDVYLOG 413
Qy      480 PIMAKIPHTDGHFHPSPLMGGFGLKNPPQILIKNTVPANPAPAFSATKPEASFTQYST 539
Db      414 PIMAKIPETGAHFPSPAMGGFGLKNPPQILIKNTVPANPAPAFSSTPVNSFTQYST 472
Qy      540 GQVSEIEMWLOKENSCKMNPVQYTSNYAKSANDFTVDNNGLYTEBRPIGT 599
Db      473 GQVTVEMWELKENSCKMNPVQYTSNYAKSANDFTVDNNGLYTEBRPIGT 532

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Search completed: November 23, 2005, 17:42:48
Job time : 29.2418 secs

CC medicament for the delivery of transgene to a host. The present sequence
CC is an AAV-1 cap protein VP3 which is useful in the production of
CC recombinant viral vector for gene delivery
XX

Sequence 534 AA;

Query Match 100.0%; Score 2906; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 8e-236;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MASGGGAPMADNNEGADGVGNASGNWCHDSWMLGDRVITTSRTMALPTYNHLYKQISS 60
DB 1 MASGGGAPMADNNEGADGVGNASGNWCHDSWMLGDRVITTSRTMALPTYNHLYKQISS 60
QY 61 ASTGASNDNHYFGYSTPMGCFDNRFHCHFSRDMORLINNNMGRPRKLNFKLNIQVK 120
DB 61 ASTGASNDNHYFGYSTPMGCFDNRFHCHFSRDMORLINNNMGRPRKLNFKLNIQVK 120
QY 121 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPOGYLTLN 180
DB 121 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPOGYLTLN 180
QY 181 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFESEVPFHSYAHQSGLDRMLNPLIDQY 240
DB 181 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFESEVPFHSYAHQSGLDRMLNPLIDQY 240
QY 241 LYYLNRTQNGSGAQNKDLFSGSPAGMSVOPKXWMLPGPCYRQORVSKTKTDNNNSNFT 300
DB 241 LYYLNRTQNGSGAQNKDLFSGSPAGMSVOPKXWMLPGPCYRQORVSKTKTDNNNSNFT 300
QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASNTALDNVMTD 360
DB 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASNTALDNVMTD 360
QY 361 EBEIKATNPVATERFGTAVAVNFQSSSTDPATGDVHAMGALPGMWQDRDVTYLOGIWAKI 420
DB 361 EBEIKATNPVATERFGTAVAVNFQSSSTDPATGDVHAMGALPGMWQDRDVTYLOGIWAKI 420
QY 421 PHTDGHFHPSPLMGGFGKLNPPPOLIKNTVPANPAPAEFSATKFASTIYOSTGOVSE 480
DB 421 PHTDGHFHPSPLMGGFGKLNPPPOLIKNTVPANPAPAEFSATKFASTIYOSTGOVSE 480
QY 481 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTIRYLRPL 534
DB 481 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTIRYLRPL 534
```

RESULT 2
AAV71168
ID AAV71168 standard; protein; 599 AA.
XX

```
AC AAV71168;
DT 08-SEP-2000 (first entry)
XX
DE Adeno-associated virus serotype 1 capsid protein VP2.
XX
KW Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
XX cap protein; recombinant viral vector; gene delivery; gene therapy;
XX vaccine; transgene; VP2.
XX
OS Adeno-associated virus 1.
XX
PN MO200028061-A2.
XX
PD 18-MAY-2000.
XX
PF 02-NOV-1999; 99WO-US025694.
XX
PR 05-NOV-1998; 98US-0107114P.
XX
PA (UYBE-) UNITV PENNSYLVANIA.
XX
```

PI Wilson JM, Xiao W;
XX
XX MPI: 2000-376571/32.
DR N-PSDB; AAD00772, AAD00778.

PT Novel adeno-associated virus serotype 1 polynucleotide useful for
PT preparation of medicament for delivery of a transgene to a host.
XX
XX
PS Claim 7; Page 93-95; 108pp; English.

CC The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA
CC which is characterized by two inverted terminal repeats (ITR) and open
CC reading frames for rep and capsid (cap) proteins. The rep reading frame
CC encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap
CC reading frame encodes three structural proteins, VP1, VP2 and VP3. The
CC AAV-1 sequence or its fragments particularly ITRs, rep and cap coding
CC regions, are useful in production of recombinant viral vectors for gene
CC delivery. These vectors can be used as gene therapy vectors, vaccine
CC vectors or antisense delivery vectors. The AAV-1 does not induce the
CC formation of neutralising antibodies specific to any serotype of AAV
CC hence is useful for transforming host cells, and in the preparation of a
CC medicament for the delivery of transgene to a host. The present sequence
CC is an AAV-1 cap protein VP2 which is useful in the production of
CC recombinant viral vector for gene delivery
XX
XX

Sequence 599 AA;

Query Match 100.0%; Score 2906; DB 3; Length 599;
Best Local Similarity 100.0%; Pred. No. 9.4e-236;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MASGGGAPMADNNEGADGVGNASGNWCHDSWMLGDRVITTSRTMALPTYNHLYKQISS 60
DB 66 MASGGGAPMADNNEGADGVGNASGNWCHDSWMLGDRVITTSRTMALPTYNHLYKQISS 125
QY 61 ASTGASNDNHYFGYSTPMGCFDNRFHCHFSRDMORLINNNMGRPRKLNFKLNIQVK 120
DB 126 ASTGASNDNHYFGYSTPMGCFDNRFHCHFSRDMORLINNNMGRPRKLNFKLNIQVK 185
QY 121 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPOGYLTLN 180
DB 186 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPOGYLTLN 245
QY 181 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFESEVPFHSYAHQSGLDRMLNPLIDQY 240
DB 246 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFESEVPFHSYAHQSGLDRMLNPLIDQY 305
QY 241 LYYLNRTQNGSGAQNKDLFSGSPAGMSVOPKXWMLPGPCYRQORVSKTKTDNNNSNFT 300
DB 306 LYYLNRTQNGSGAQNKDLFSGSPAGMSVOPKXWMLPGPCYRQORVSKTKTDNNNSNFT 365
QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASNTALDNVMTD 360
DB 366 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGVMIFGKESAGASNTALDNVMTD 425
QY 361 EBEIKATNPVATERFGTAVAVNFQSSSTDPATGDVHAMGALPGMWQDRDVTYLOGIWAKI 420
DB 426 EBEIKATNPVATERFGTAVAVNFQSSSTDPATGDVHAMGALPGMWQDRDVTYLOGIWAKI 485
QY 421 PHTDGHFHPSPLMGGFGKLNPPPOLIKNTVPANPAPAEFSATKFASTIYOSTGOVSE 480
DB 486 PHTDGHFHPSPLMGGFGKLNPPPOLIKNTVPANPAPAEFSATKFASTIYOSTGOVSE 545
QY 481 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTIRYLRPL 534
DB 546 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTIRYLRPL 599
```

RESULT 3
AAV71167
ID AAV71167 standard; protein; 736 AA.
XX
XX AAV71167;
AC

XX 08-SEP-2000 (first entry)
 DT Adeno-associated virus serotype 1 capsid protein vp1.
 XX
 DE Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
 XX Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
 KM cap protein; recombinant viral vector; gene delivery; gene therapy;
 KM vaccine; transgene; VPI.
 XX
 OS Adeno-associated virus 1.
 XX
 PN WO200028061-A2.
 XX
 PD 18-MAY-2000.
 XX
 XX 02-NOV-1999; 99WO-US025694.
 PF
 XX 05-NOV-1998; 98US-0107114P.
 PR
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 PA Wilson JM, Xiao W;
 PI WPI; 2000-376571/32.
 DR N-PSDB; AAD00772, AAD00777.
 XX
 XX Novel adeno-associated virus serotype 1 polynucleotide useful for
 PT preparation of medicament for delivery of a transgene to a host.
 XX
 PS Claim 7; Page 87-90; 108bp; English.
 XX
 CC The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA
 CC which is characterised by two inverted terminal repeats (ITR) and open
 CC reading frames for rep and capsid (cap) proteins. The rep reading frame
 CC encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap
 CC reading frame encodes three structural proteins, VP1, VP2 and VP3. The
 CC AAV-1 sequence or its fragments particularly ITRs, rep and cap coding
 CC regions, are useful in production of recombinant viral vectors for gene
 CC delivery. These vectors can be used as gene therapy vectors, vaccine
 CC vectors or antisense delivery vectors. The AAV-1 does not induce the
 CC formation of neutralising antibodies specific to any serotype of AAV
 CC hence is useful for transforming host cells, and in the preparation of a
 CC medicament for the delivery of transgene to a host. The present sequence
 CC is an AAV-1 cap protein VPI which is useful in the production of
 CC recombinant viral vector for gene delivery
 CC
 XX Sequence 736 AA;
 SQ
 Query Match 100.0%; Score 2906; DB 3; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.3e-235;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGAPADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLYKOISS 60
 DB 203 MASGGAPADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLYKOISS 262
 QY 61 ASTGASNDNHFGYSTPWFYDFENRPFCHSPRDWRLINNNNGFRKRLNFKLNFIOVK 120
 DB 263 ASTGASNDNHFGYSTPWFYDFENRPFCHSPRDWRLINNNNGFRKRLNFKLNFIOVK 322
 QY 121 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLSAHOGLPPPADVFMIPQYGYLTIN 180
 DB 323 EVTTNDGVTTIANNLSTVQVFSDEYQLPYVLSAHOGLPPPADVFMIPQYGYLTIN 382
 QY 181 NSGQAVRSGSFYCLEYFSPQMLRTGNNFTSYTFEESVPHSSVYHSSQSLDRMLNPLIDQY 240
 DB 383 NSGQAVRSGSFYCLEYFSPQMLRTGNNFTSYTFEESVPHSSVYHSSQSLDRMLNPLIDQY 442
 QY 241 LYYINRPNONGSGAKNDLLFSRGS PAGMSVQPKMILPGPCYRQQRVSKTKTDNNNSNFT 300
 DB 443 LYYINRPNONGSGAKNDLLFSRGS PAGMSVQPKMILPGPCYRQQRVSKTKTDNNNSNFT 502
 QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 360

DB 503 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 562
 QY 361 EEEIKATNPVATERFGTAAVNFQSSSTDPATGDVHAMGALPGMWQDRDVIYQGPIMAKI 420
 DB 563 EEEIKATNPVATERFGTAAVNFQSSSTDPATGDVHAMGALPGMWQDRDVIYQGPIMAKI 622
 QY 421 PHTDGHFHPSPLMGFGGLKNPPQILLIKNTVPAPPAEFSAFKFASFTIOYSTGOVSVE 480
 DB 623 PHTDGHFHPSPLMGFGGLKNPPQILLIKNTVPAPPAEFSAFKFASFTIOYSTGOVSVE 682
 QY 481 IEMELOKENSKRWNPVOYTSNYAKSAAVDFVDNNGLYTEBRPIGTRVLTREPL 534
 DB 683 IEMELOKENSKRWNPVOYTSNYAKSAAVDFVDNNGLYTEBRPIGTRVLTREPL 736

RESULT 4
 ABB80232
 ID ABB80232 standard; protein; 736 AA.
 XX
 AC ABB80232;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE AAV1 vp1 protein.
 XX
 XX Adeno-associated virus; AAV; serotype 9; rep; cap; vp1; vp2; vp3;
 KM splice variant; transgene.
 OS
 XX Adeno associated virus serotype 1.
 XX
 PN WO2003052052-A2.
 XX
 PD 26-JUN-2003.
 XX
 PF 12-NOV-2002; 2002WO-US033631.
 XX
 PR 17-DEC-2001; 2001US-0341150P.
 PR 05-JUN-2002; 2002US-0386132P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Gao G, Wilson JM, Alvira M;
 PT WPI; 2003-523523/49.
 DR
 XX
 XX New isolated adeno-associated virus (AAV) comprising an AAV9 capsid,
 PT useful for preparing a medicament for delivering a transgene to a cell.
 PS Disclosure; Fig 2; 76pp; English.
 XX
 CC The sequences given in ABB80231-34 represent vp1 proteins derived from
 CC various adeno-associated virus (AAV) serotypes. These sequences were used
 CC in the scope of the invention for comparison with the cap protein derived
 CC from AAV serotype 9. The AAV capsid comprises three proteins vp1, vp2 and
 CC vp3, which are alternative splice variants. The AAV or the nucleic acid
 CC molecule is useful for preparing a medicament for delivering a transgene
 CC to a cell
 CC
 XX Sequence 736 AA;
 SQ
 Query Match 100.0%; Score 2906; DB 6; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.3e-235;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGAPADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLYKOISS 60
 DB 203 MASGGAPADNNEGADGVGNASGNHCDSTWLGDRVITTSRTWALPTYNHLYKOISS 262
 QY 61 ASTGASNDNHFGYSTPWFYDFENRPFCHSPRDWRLINNNNGFRKRLNFKLNFIOVK 120
 DB 263 ASTGASNDNHFGYSTPWFYDFENRPFCHSPRDWRLINNNNGFRKRLNFKLNFIOVK 322

QY 121 EVTTNDGVTITANNLTSTVQVFSDESEYQLPYVLGSAHOGCLPPPADVFMIPOYGYLTIN 180
 Db 323 EVTTNDGVTITANNLTSTVQVFSDESEYQLPYVLGSAHOGCLPPPADVFMIPOYGYLTIN 382
 QY 181 NGSOAVGRSSFYCLEYFPPSQMLRTGNNTFTSYTFEEVPHSSYAHSGSLDRLMPLIDQY 240
 Db 383 NGSOAVGRSSFYCLEYFPPSQMLRTGNNTFTSYTFEEVPHSSYAHSGSLDRLMPLIDQY 442
 QY 241 LYYLNRTNONGSAGNKKLLFSGSPAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
 Db 443 LYYLNRTNONGSAGNKKLLFSGSPAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 502
 QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGWMIFGKESAGASNTALDVMITD 360
 Db 503 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGWMIFGKESAGASNTALDVMITD 562
 QY 361 EBEIKATNPVATERGTYAVANFQSSSTDPATGDVHAMGALPGMWQODRDVYLQGPIMAKI 420
 Db 563 EBEIKATNPVATERGTYAVANFQSSSTDPATGDVHAMGALPGMWQODRDVYLQGPIMAKI 622
 QY 421 PHTDGHFHPSPLMGSGFGLKNPPQILIKNTVPANPAPAFSATKFASTITQYSGQSV 480
 Db 623 PHTDGHFHPSPLMGSGFGLKNPPQILIKNTVPANPAPAFSATKFASTITQYSGQSV 682
 QY 481 IEMELQKNSKRMNPEVOYTSNYAKSANVDFTVNNGLYTBPRPIGTRYLTRPL 534
 Db 683 IEMELQKNSKRMNPEVOYTSNYAKSANVDFTVNNGLYTBPRPIGTRYLTRPL 736

RESULT 5
 ABR62762
 ID ABR62762 standard; protein; 736 AA.

AC ABR62762;

DT 06-NOV-2003 (first entry)

DE Adeno associated virus 1 capsid protein vpl.

KM AAV, AAV1, capsid; vector; gene therapy; antisense therapy; vaccine.

OS Adeno associated virus.

PN WO2003052051-A2.

XX 26-JUN-2003.

PF 12-NOV-2002; 2002WO-US033630.

PR 17-DEC-2001; 2001US-0341151P.

PR 01-MAY-2002; 2002US-0377133P.

PR 05-JUN-2002; 2002US-0386122P.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Gao G, Wilson JM, Alvirra M;

DR MPI; 2003-523522/49.

PT New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.

XX Disclosure; Fig 2A-C; 82pp; English.

CC The present sequence is the protein sequence of the vpl capsid protein of adeno associated virus serotype 1 (AAV1). The invention provides the CC nucleic acid and amino acid sequences of novel AAV8 and fragments of CC these sequences. Each of these fragments may be used in a variety of CC vector systems and host cells. Among the desirable fragments are the cap CC proteins, including vpl, vp2, vp3 and hypervariable regions, the rep CC proteins, including rep78, rep68, rep52 and rep40, and the sequences CC encoding these proteins. The fragments may be used alone, in combination

CC with other AAV8 sequences or in combination with elements from other AAV CC or non-AAV viral sequences in the production of recombinant AAV and for CC use as antisense delivery vectors; gene therapy vectors or vaccine CC vectors. A claimed molecule comprises a cap protein of a functional AAV CC rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and CC AAV6
 XX
 SQ Sequence 736 AA;

Query Match 100.0%; Score 2906; DB 7; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.3e-235;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGA PMADNNGADGVGNASGNMHCDSWMLGDRVITTSRTMALPTYNHLYKQISS 60
 Db 203 MASGGA PMADNNGADGVGNASGNMHCDSWMLGDRVITTSRTMALPTYNHLYKQISS 262
 QY 61 ASTGASNDNHFGYSTPMGYDFNRFCHFSRDMQRLINNMGFRPRKLNFKLFNIQVK 120
 Db 263 ASTGASNDNHFGYSTPMGYDFNRFCHFSRDMQRLINNMGFRPRKLNFKLFNIQVK 322
 QY 121 EVTTNDGVTITANNLTSTVQVFSDESEYQLPYVLGSAHOGCLPPPADVFMIPOYGYLTIN 180
 Db 323 EVTTNDGVTITANNLTSTVQVFSDESEYQLPYVLGSAHOGCLPPPADVFMIPOYGYLTIN 382
 QY 181 NGSOAVGRSSFYCLEYFPPSQMLRTGNNTFTSYTFEEVPHSSYAHSGSLDRLMPLIDQY 240
 Db 383 NGSOAVGRSSFYCLEYFPPSQMLRTGNNTFTSYTFEEVPHSSYAHSGSLDRLMPLIDQY 442
 QY 241 LYYLNRTNONGSAGNKKLLFSGSPAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
 Db 443 LYYLNRTNONGSAGNKKLLFSGSPAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 502
 QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGWMIFGKESAGASNTALDVMITD 360
 Db 503 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGSGWMIFGKESAGASNTALDVMITD 562
 QY 361 EBEIKATNPVATERGTYAVANFQSSSTDPATGDVHAMGALPGMWQODRDVYLQGPIMAKI 420
 Db 563 EBEIKATNPVATERGTYAVANFQSSSTDPATGDVHAMGALPGMWQODRDVYLQGPIMAKI 622
 QY 421 PHTDGHFHPSPLMGSGFGLKNPPQILIKNTVPANPAPAFSATKFASTITQYSGQSV 480
 Db 623 PHTDGHFHPSPLMGSGFGLKNPPQILIKNTVPANPAPAFSATKFASTITQYSGQSV 682
 QY 481 IEMELQKNSKRMNPEVOYTSNYAKSANVDFTVNNGLYTBPRPIGTRYLTRPL 534
 Db 683 IEMELQKNSKRMNPEVOYTSNYAKSANVDFTVNNGLYTBPRPIGTRYLTRPL 736

RESULT 6
 ADE76565
 ID ADE76565 standard; protein; 736 AA.

AC ADE76565;

DT 29-JAN-2004 (first entry)

DE Adeno-associated virus (AAV) related protein, SEQ ID No 64.

KM adeno-associated virus; AAV; cytosolic; antipoxviral; antirheumatic;

KM antitachytic; neuroprotective; antidiabetic; antithyroid;

KM dermatologic; antiinflammatory; gene therapy; vaccine;

KM hyperproliferative; cancer; psoriasis; autoimmune disease;

KM rheumatoid arthritis; multiple sclerosis; diabetes;

OS autoimmune thyroiditis; scleroderma; Crohn's disease.

XX Undifferentiated.
 XX BP1310571-A2.
 XX 14-MAY-2003.
 XX

PF 12-NOV-2002; 2002EP-00257826.
 XX 13-NOV-2001; 2001US-0350607P.
 PR 17-DEC-2001; 2001US-0341117P.
 PR 01-MAY-2002; 2002US-0377066P.
 PR 05-JUN-2002; 2002US-0386755P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX PA
 XX PI
 XX Gao G, Wilson JM, Alvira M;
 DR WPI; 2003-450984/43.
 XX
 PT Detecting adeno-associated virus sequences in a sample, useful for e.g.
 PT preventing or treating hyperproliferative or autoimmune diseases,
 PT comprising subjecting a sample having a DNA to amplification via
 PT polymerase chain reaction.
 XX
 PS Disclosure; SEQ ID NO 64; 419pp; English.
 XX
 XX The invention relates to a novel method for detecting adeno-associated
 CC virus (AAV) sequences in a sample, which comprises subjecting a sample
 CC containing a DNA to amplification via a polymerase chain reaction (PCR).
 CC The AAV sequence have the following activities: cytostatic,
 CC antiproliferative, antitumor, antidiabetic, neuroprotective,
 CC antidiabetic, antihypertensive, dermatological, and anti-inflammatory. The AAV
 CC sequence can be used in gene therapy or as part of a vaccine to treat
 CC disorders. The method is useful in detecting and/or identifying AAV
 CC sequences and isolating novel sequences that are identifying. The
 CC sequences may be used e.g. for preventing or treating hyperproliferative
 CC conditions such as cancers and psoriasis, and other autoimmune diseases
 CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
 CC chondritis, scleroderma or Crohn's disease. This sequence represents an
 CC AAV related protein sequence of the invention.
 XX
 XX Sequence 736 AA;
 SQ

Query Match 100.0%; Score 2906; DB 7; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.3e-235;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWALPTNNHLYQISS 60
 DB 203 MASGGGAPMADNNEGADGVGNASGNHCDSTWLGDRVITTTSTWALPTNNHLYQISS 262
 QY 61 ASTGASNDNHFGYSTPMWGFDFNRFFCHSPRDMORLNNNGFPRKLNFLPNIOVK 120
 DB 263 ASTGASNDNHFGYSTPMWGFDFNRFFCHSPRDMORLNNNGFPRKLNFLPNIOVK 322
 QY 121 EYTTNDGVTITANNLTSTVOVFSDESEYQLPYVLSAHOGLPPFPADVEMIPOYGYLTIN 180
 DB 323 EYTTNDGVTITANNLTSTVOVFSDESEYQLPYVLSAHOGLPPFPADVEMIPOYGYLTIN 382
 QY 181 NSGQAVGRSSFCLEYPFSQMLRTGNFTSYTFEEVPHSSVAHSQSLDRMLNPLIDQY 240
 DB 383 NSGQAVGRSSFCLEYPFSQMLRTGNFTSYTFEEVPHSSVAHSQSLDRMLNPLIDQY 442
 QY 241 LYTINFRONOSGSAONKDLLFSRGSPPAGSVOPKNMIPGCVYQORRSKTKTNNNSNFT 300
 DB 443 LYTINFRONOSGSAONKDLLFSRGSPPAGSVOPKNMIPGCVYQORRSKTKTNNNSNFT 502
 QY 301 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMGSMVIFGKESAGASNTALDNWITD 360
 DB 503 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMGSMVIFGKESAGASNTALDNWITD 562
 QY 361 EEBIKATNPVATERFGVAVNFOSSSTDPATGDVHANALPGMWQORRVYLLQGPVIAKI 420
 DB 563 EEBIKATNPVATERFGVAVNFOSSSTDPATGDVHANALPGMWQORRVYLLQGPVIAKI 622
 QY 421 PHTDGHHPSPLMGFGGLKNPPOIILKNPVPANPAEFSATFASFITIOYSTGOVSVE 480
 DB 623 PHTDGHHPSPLMGFGGLKNPPOIILKNPVPANPAEFSATFASFITIOYSTGOVSVE 682

QY 481 IEMELÖKENSRRKNPEVOYTSNYAKSANVDFVNDNGGTYTEBRPIGTRVLRPL 534
 DB 683 IEMELÖKENSRRKNPEVOYTSNYAKSANVDFVNDNGGTYTEBRPIGTRVLRPL 736
 RESULT 7
 ADV70294
 ID ADV70294 standard; protein; 736 AA.
 AC ADV70294;
 XX
 XX
 XX
 DT 10-MAR-2005 (first entry)
 XX
 XX
 DE Primate adeno-associated virus 1 capsid protein VP1.
 XX
 XX immunosuppressive; gene therapy; immunogenicity; virus inactivation;
 KW hemophilia; Pepck deficiency; galactosemia; phenylketonuria;
 KW Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
 KW atherosclerosis; thrombosis; embolism; Parkinson's disease;
 KW congestive heart failure; cancer; inflammation; immune disorder;
 KW muscular dystrophy; diabetes; VPL.
 XX
 XX Adeno-associated virus 1.
 OS
 XX
 XX
 PN MO2004112727-A2.
 XX
 XX
 PD 29-DEC-2004.
 XX
 XX
 PF 21-JUN-2004; 2004WO-US019884.
 XX
 XX
 PR 19-JUN-2003; 2003US-0480395P.
 PR 30-APR-2004; 2004US-0567310P.
 PR 03-JUN-2004; 2004US-0576501P.
 XX
 XX (AVIG-) AVIGEN INC.
 PA
 PI Arbetman AE, Colosi P, Lochrie MA, Surosky RT;
 XX
 XX WPI; 2005-048755/05.
 DR
 XX
 PT New mutated adeno-associated virus (AAV) capsid protein that when present
 PT in an AAV virion imparts decreased immunoreactivity to the virion as
 PT compared to the corresponding wild-type virion, useful for treating e.g.
 PT hemophilia.
 XX
 XX
 PS Example 5; SEQ ID NO 20; 136pp; English.
 PS
 XX
 CC The invention describes a mutated adeno-associated virus (AAV) capsid
 CC protein that when present in an AAV virion imparts decreased
 CC immunoreactivity to the virion as compared to the corresponding wild-type
 CC virion. Also described are: a polynucleotide encoding the mutated protein
 CC above; a recombinant AAV virion comprising the mutated protein above; and
 CC delivering a recombinant AAV virion to a cell or tissue of a vertebrate
 CC subject. The recombinant AAV virion is useful for delivering a
 CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate
 CC subject, where the protein encoded by the heterologous nucleic acid
 CC molecule is expressed at a level that provides a therapeutic effect,
 CC where the recombinant AAV virion may comprise a non-primate, mammalian
 CC AAV capsid protein that when present in an AAV virion imparts decreased
 CC immunoreactivity to the virion as compared to immunoreactivity of primate
 CC AAV-2, and the heterologous nucleic acid molecule, where the heterologous
 CC nucleic acid molecule encodes a therapeutic protein and is operably
 CC linked to control elements capable of directing the in vivo transcription
 CC and translation of the protein. The protein of the recombinant AAV virion
 CC is useful for treating or preventing a wide variety of disorders such as
 CC hemophilia, glycogen storage deficiency type 1A, Pepck deficiency,
 CC galactosemia, phenylketonuria, Crigler-Najjar disease, Gout and Lesch-
 CC Nyhan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis,
 CC thrombosis, embolisms, Parkinson's disease, congestive heart failure,
 CC cancer, inflammatory and immune disorders, muscular dystrophies, and
 CC diabetes. This is the amino acid sequence of adeno-associated virus 1
 CC (AAV) capsid protein VP1.
 XX

XX Adeno-associated virus protein SEQ ID NO 162.
 DE rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 XX scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 XX bacterial infection; cancer; ulcerative colitis; antirheumatic;
 XX antiarthritic; neutropenic; antineoplastic; antidiabetic;
 XX antiparasitic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
 XX virucide; antibacterial; cytostatic; antitumor; dermatological.
 OS Adeno-associated virus.
 XX WO200503321-A2.
 XX 14-APR-2005.
 XX 30-SEP-2004; 2004WO-US028817.
 XX 30-SEP-2003; 2003US-0508226P.
 XX 29-APR-2004; 2004US-0566546P.
 XX (UYPE-) UNIT PENNSYLVANIA.
 XX Wilson JM, Gao G, Alvira MR, Vandenberghe LH;
 PI MPI; 2005-285437/29.
 XX New adeno-associated virus (AAV) clade comprising at least three AAV
 PT members, useful for preventing and/or treating arthritis, multiple
 PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
 PT infection and cancer.
 XX Disclosure; SEQ ID NO 162; 569pp; English.
 XX The invention relates to an adeno-associated virus (AAV) clade comprising
 CC at least three AAV members, where each member of the AAV clade is
 CC phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX Sequence 736 AA;
 SQ
 Query Match 100.0%; Score 2906; DB 9; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.3e-235;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGGAPMADNNEGADGVGNAGNHCDSITWIGDRITTTSTTWMALPTYNHLYKOISS 60
 DB 203 MASGGAPMADNNEGADGVGNAGNHCDSITWIGDRITTTSTTWMALPTYNHLYKOISS 262
 QY 61 ASGASNDNHYFGYSTPMGTFDFNRFCHSPRDQRLINNNGFRKRLNFKLNIQVK 120
 DB 263 ASGASNDNHYFGYSTPMGTFDFNRFCHSPRDQRLINNNGFRKRLNFKLNIQVK 322
 QY 121 EVTTNDGVTTIANNLSTVOVFSDBEYQLPYVLGSAHQGLPEPPADVFMIPQGYLTIN 180
 DB 323 EVTTNDGVTTIANNLSTVOVFSDBEYQLPYVLGSAHQGLPEPPADVFMIPQGYLTIN 382
 QY 181 NGGAVRSGSFYCLIEFPSCMLRTGNNFTSYTEEPFSSVAHSGSLRLNMLDQY 240
 DB 383 NGGAVRSGSFYCLIEFPSCMLRTGNNFTSYTEEPFSSVAHSGSLRLNMLDQY 442
 QY 241 LYYNTRTONSGSQNDLLFSRSGPAGMSVQPKMILPGPCYRQORSKTKTDNNNSNFT 300
 DB 443 LYYNTRTONSGSQNDLLFSRSGPAGMSVQPKMILPGPCYRQORSKTKTDNNNSNFT 502
 QY 301 WTGASKYLNLRGRESINIPGTAMASHKDEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 360

DB 503 WTGASKYLNLRGRESINIPGTAMASHKDEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 562
 QY 361 EEEIKATNPVATERFGTAAVNFQSSSTDPATCDVHAMGALPGMWQDRDVIYQGPIMAKI 420
 DB 563 EEEIKATNPVATERFGTAAVNFQSSSTDPATCDVHAMGALPGMWQDRDVIYQGPIMAKI 622
 QY 421 PHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSATITQYSTGVSV 480
 DB 623 PHTDGHFHPSPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSATITQYSTGVSV 682
 QY 481 IEMELQKENSRRWNPDEVQYTSNYAKSANVDFVDNNGLYTEBRPIGTRYLTRPL 534
 DB 683 IEMELQKENSRRWNPDEVQYTSNYAKSANVDFVDNNGLYTEBRPIGTRYLTRPL 736
 RESULT 10
 ADV67506
 ID ADV67506 standard; protein; 735 AA.
 XX ADV67506;
 AC 10-MAR-2005 (first entry)
 DT 10-MAR-2005 (first entry)
 XX Amino acid sequence of the capsid protein of AAV serotype 1.
 XX antiarteriosclerotic; antilipemic; gene therapy; cholesterol;
 KW apolipoprotein E; apoE; apolipoprotein A; apoA; atherosclerosis;
 KW lipoprotein defect; capsid protein.
 XX Adeno-associated virus.
 XX WO2004108922-A2.
 XX 16-DEC-2004.
 XX 23-APR-2004; 2004WO-US010965.
 XX 25-APR-2003; 2003US-0465293P.
 XX (UYPE-) UNIT PENNSYLVANIA.
 XX Rader DJ, Wilson JM;
 PI MPI; 2005-031700/03.
 XX Lowering total cholesterol levels and treating atherosclerosis in a
 PT subject comprises delivering a recombinant adeno-associated virus (AAV)
 PT comprising an AAV serotype capsid protein or a gene encoding human
 PT apolipoprotein E (apoE) or apoA.
 PS Disclosure; SEQ ID NO 4; 69pp; English.
 XX The specification describes a method for lowering total cholesterol
 CC levels in a subject. The method comprises delivering to the subject a
 CC recombinant adeno-associated virus (AAV) comprising a gene encoding a
 CC human apolipoprotein E (apoE) or apoA under the control of a regulatory
 CC control sequence which directs expression of the gene. The recombinant
 CC AAV also comprises a capsid protein selected from an AAV serotype (e.g.,
 CC AAV7 or AAV8) which preferentially expresses high levels of transgene in
 CC live. A therapeutically effective amount of apoE or apoA expression is
 CC obtained upon delivery of low dose of AAV. The method of the invention is
 CC useful for lowering total cholesterol levels in a subject, e.g., for
 CC treating atherosclerosis, and for correcting defects in lipoprotein. The
 CC present sequence represents a capsid protein of AAV serotype 1 (AAV1),
 CC which may be used in recombinant AAV vectors of the invention.
 XX Sequence 735 AA;
 SQ
 Query Match 99.9%; Score 2902; DB 9; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.8e-235;
 Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MASGGAGPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTWALPTYNHLYKQISS 60
Db 203 MASGGAGPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTWALPTYNHLYKQISS 262
OY 61 ASTGASNDNHFGYSTPMGCFDFFNRFCHFSFPRDMQRLINNMGFRPRKLNFKLFNIQVK 120
Db 263 ASTGASNDNHFGYSTPMGCFDFFNRFCHFSFPRDMQRLINNMGFRPRKLNFKLFNIQVK 322
OY 121 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQGCLPPPADVFMIPOYGYLTLN 180
Db 323 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQGCLPPPADVFMIPOYGYLTLN 382
OY 181 NGSQAVGRSSFYCLEYFSPSQMLRTGNNTFFSYTFEEVPHSSVYAHSSQSLDRIMNPDIQY 240
Db 363 NGSQAVGRSSFYCLEYFSPSQMLRTGNNTFFSYTFEEVPHSSVYAHSSQSLDRIMNPDIQY 442
OY 241 LYYLNRTONOGSSAONKDLFSRGSFAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
Db 443 LYYLNRTONOGSSAONKDLFSRGSFAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSNFT 502
OY 301 WTGASKYLNNGRESITINPGTAMASHKDEDEKFFPMGVMIFGKSASAGSNTALDNVMTTD 360
Db 503 WTGASKYLNNGRESITINPGTAMASHKDEDEKFFPMGVMIFGKSASAGSNTALDNVMTTD 562
OY 563 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMTWQODRDVYLQGPIMAKI 420
Db 622 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMTWQODRDVYLQGPIMAKI 622
OY 421 PHTDGHFHPSPLMGFGKLPNPOLLIKNTVPANPAPFAFATKASFTITQYSTQGVSE 480
Db 623 PHTDGHFHPSPLMGFGKLPNPOLLIKNTVPANPAPFAFATKASFTITQYSTQGVSE 682
OY 481 IEMELQKENSKRMPNEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTXYLTRPL 533
Db 683 IEMELQKENSKRMPNEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTXYLTRPL 735

RESULT 11
AD227008
ID AD227008 standard; protein, 736 AA.
XX
AC AD227008;
XX
DT 30-JUN-2005 (first entry)
XX
DE Adeno-associated virus protein SEQ ID NO 158.
XX
KW rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
KW scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
KW bacterial infection; cancer; ulcerative colitis; anti-inflammatory;
KW antiarthritis; neuroprotective; antiinflammatory; antidiabetic;
KW antipsoriatic; vasotrophic; gastrointestinal-gen.; hemostatic; anti-HIV;
KW virucide; antibacterial; cytostatic; antitumor; dermatological.
XX
OS Adeno-associated virus.
XX
PN MO200503321-A2.
XX
PD 14-APR-2005.
XX
PF 30-SEP-2004; 2004MO-US028817.
XX
PR 30-SEP-2003; 2003US-0508226P.
XX
PR 29-APR-2004; 2004US-0566546P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Wilson JM, Gao G, Alvira MR, Vandenberghe LH;
XX
DR WPI; 2005-285437/29.
XX
PT New adeno-associated virus (AAV) clade comprising at least three AAV
members, useful for preventing and/or treating arthritis, multiple
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PT sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
PT infection and cancer.
XX
PS Claim 19; SEQ ID NO 158; 569pp; English.
XX
CC The invention relates to an adeno-associated virus (AAV) clade comprising
CC at least three AAV members, where each member of the AAV clade is
CC phylogenetically related as determined using a Neighbor-Joining heuristic
CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
CC correction distance measurement of no more than 0.05. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
CC colitis. The present sequence represents the amino acid sequence of an
CC adeno-associated virus protein.
XX
SQ Sequence 736 AA;
XX
Query Match 99.5%; Score 2892; DB 9; Length 736;
Beat Local Similarity 99.6%; Pred. No. 1.9e-234;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 MASGGAGPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTWALPTYNHLYKQISS 60
Db 203 MASGGAGPMADNNEGADGVGNASGNMHCDSITWLGDRVITTTSTRTWALPTYNHLYKQISS 262
OY 61 ASTGASNDNHFGYSTPMGCFDFFNRFCHFSFPRDMQRLINNMGFRPRKLNFKLFNIQVK 120
Db 263 ASTGASNDNHFGYSTPMGCFDFFNRFCHFSFPRDMQRLINNMGFRPRKLNFKLFNIQVK 322
OY 121 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQGCLPPPADVFMIPOYGYLTLN 180
Db 323 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQGCLPPPADVFMIPOYGYLTLN 382
OY 181 NGSQAVGRSSFYCLEYFSPSQMLRTGNNTFFSYTFEEVPHSSVYAHSSQSLDRIMNPDIQY 240
Db 363 NGSQAVGRSSFYCLEYFSPSQMLRTGNNTFFSYTFEEVPHSSVYAHSSQSLDRIMNPDIQY 442
OY 241 LYYLNRTONOGSSAONKDLFSRGSFAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
Db 443 LYYLNRTONOGSSAONKDLFSRGSFAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSNFT 502
OY 301 WTGASKYLNNGRESITINPGTAMASHKDEDEKFFPMGVMIFGKSASAGSNTALDNVMTTD 360
Db 503 WTGASKYLNNGRESITINPGTAMASHKDEDEKFFPMGVMIFGKSASAGSNTALDNVMTTD 562
OY 563 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMTWQODRDVYLQGPIMAKI 420
Db 622 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMTWQODRDVYLQGPIMAKI 622
OY 421 PHTDGHFHPSPLMGFGKLPNPOLLIKNTVPANPAPFAFATKASFTITQYSTQGVSE 480
Db 623 PHTDGHFHPSPLMGFGKLPNPOLLIKNTVPANPAPFAFATKASFTITQYSTQGVSE 682
OY 481 IEMELQKENSKRMPNEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTXYLTRPL 534
Db 683 IEMELQKENSKRMPNEVOYTSNYAKSANDFTVDNNGLYTEBRPIGTXYLTRPL 736

RESULT 12
AD227086
ID AD227086 standard; protein, 737 AA.
XX
AC AD227086;
XX
DT 30-JUN-2005 (first entry)
XX
DE Adeno-associated virus protein SEQ ID NO 236.
XX
KW rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
KW scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
KW bacterial infection; cancer; ulcerative colitis; antiinflammatory;
```

KM antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
 KM antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
 KM virucide; antibacterial; cyostatic; antitumor; dermatological.
 OS Adeno-associated virus.
 FM WO2005033321-A2.
 PM 14-APR-2005.
 PD 30-SEP-2004; 2004WO-US028817.
 PF 30-SEP-2003; 2003US-0508226P.
 PR 29-APR-2004; 2004US-0566546P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Wilson JM, Gao G, Alvira MR, Vandenberghe LH;
 PI WPI; 2005-285437/29.
 DR The invention relates to an adeno-associated virus (AAV) clade comprising
 XX at least three AAV members, where each member of the AAV clade is
 XX phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX
 XX
 SQ Sequence 737 AA;
 Query Match 99.4%; Score 2892; DB 9; Length 737;
 Best Local Similarity 99.4%; Pred. No. 1.9e-234;
 Matches 531; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASGGAPADNNEGADVGNASGNWCHDSTWLGDRVITTTSTRTWALPTYNHLYKQISS 60
 DB 204 MAAGGAPADNNEGADVGNASGNWCHDSTWLGDRVITTTSTRTWALPTYNHLYKQISS 263
 QY 61 ASGASNDNHYFGYSTPMGFFDFNRFCHSPRDMQRLINNNNGFRPKRLNPLFNIOVK 120
 DB 264 ASGASNDNHYFGYSTPMGFFDFNRFCHSPRDMQRLINNNNGFRPKRLNPLFNIOVK 323
 QY 121 EVTTNDGVTTIANNLSTGVFSDSEYQALPYVLSAHOGLPPPADVEMIPQYGYLTN 180
 DB 324 EVTTNDGVTTIANNLSTGVFSDSEYQALPYVLSAHOGLPPPADVEMIPQYGYLTN 383
 QY 181 NSQAVGRSSFFCLEYFSPQMLRTGNFTSYTFEVPFHSVAHSQSLDLRLNPLIDQY 240
 DB 384 NSQAVGRSSFFCLEYFSPQMLRTGNFTSYTFEVPFHSVAHSQSLDLRLNPLIDQY 443
 QY 241 LYYLNRTONSGSNONDLFFSRGSPAGMSVOPKMLPGCYRQQRVSKTDTNNNSNFT 300
 DB 444 LYYLNRTONSGSNONDLFFSRGSPAGMSVOPKMLPGCYRQQRVSKTDTNNNSNFT 503
 QY 301 WTGASKYNLNGRESIINPGTAMASHKDDKFFPMGVMIPGKESAGASNTALDNWITD 360
 DB 504 WTGASKYNLNGRESIINPGTAMASHKDDKFFPMGVMIPGKESAGASNTALDNWITD 563
 QY 361 EEEIKANNPYATPEFGVAVNFOSSSTDPATGDVHAMGALPGWVQORDVYLGSPITAKI 420
 DB 564 EEEIKANNPYATPEFGVAVNFOSSSTDPATGDVHAMGALPGWVQORDVYLGSPITAKI 623

QY 421 PHTDGHFPHSPMLMGFGGLKNPPQILIKNTVPANPPAEFSATKFSFILOYSGOVSE 480
 DB 624 PHTDGHFPHSPMLMGFGGLKNPPQILIKNTVPANPPAEFSATKFSFILOYSGOVSE 683
 QY 481 IEMELOKENSKRMNPEVOYTSNYAKSANVDFVDDNNGLYTEPRPIGTRYLTPPL 534
 DB 684 IEMELOKENSKRMNPEVOYTSNYAKSANVDFVDDNNGLYTEPRPIGTRYLTPPL 737
 RESULT 13
 AD227074
 ID AD227074 strand; protein; 736 AA.
 AC AD227074;
 XX 30-JUN-2005 (first entry)
 DE Adeno-associated virus protein SEQ ID NO 224.
 XX
 XX rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
 KW scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
 KW bacterial infection; cancer; ulcerative colitis; antineumatic;
 KW antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
 KW antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
 KW virucide; antibacterial; cyostatic; antitumor; dermatological.
 XX
 OS Adeno-associated virus.
 XX
 XX
 PN WO2005033321-A2.
 PD 14-APR-2005.
 PF 30-SEP-2004; 2004WO-US028817.
 PR 30-SEP-2003; 2003US-0508226P.
 PR 29-APR-2004; 2004US-0566546P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Wilson JM, Gao G, Alvira MR, Vandenberghe LH;
 PI WPI; 2005-285437/29.
 DR The invention relates to an adeno-associated virus (AAV) clade comprising
 XX at least three AAV members, where each member of the AAV clade is
 XX phylogenetically related as determined using a Neighbor-Joining heuristic
 CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
 CC correction distance measurement of no more than 0.05. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
 CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
 CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
 CC colitis. The present sequence represents the amino acid sequence of an
 CC adeno-associated virus protein.
 XX
 XX
 SQ Sequence 736 AA;
 Query Match 99.4%; Score 2888; DB 9; Length 736;
 Best Local Similarity 99.4%; Pred. No. 4.2e-234;
 Matches 531; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MASGGAPADNNEGADVGNASGNWCHDSTWLGDRVITTTSTRTWALPTYNHLYKQISS 60
 DB 203 MASGGAPADNNEGADVGNASGNWCHDSTWLGDRVITTTSTRTWALPTYNHLYKQISS 262

```

QY 61 ASTGASNDNHFGYSTPWGYDFPNRFCHFSRPRDQRLINNNGFRPKRLNFKLFINIQVK 120
DB 263 ASTGASNDNHFGYSTPWGYDFPNRFCHFSRPRDQRLINNNGFRPKRLNFKLFINIQVK 322
QY 121 EYTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHQGLPPRPADVFMIPQGYLTILN 180
DB 323 EYTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHQGLPPRPADVFMIPQGYLTILN 382
QY 181 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSYTFEEVPHSSVYHSSQSLDRLMPLIDQY 240
DB 383 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSYTFEEVPHSSVYHSSQSLDRLMPLIDQY 442
QY 241 LYYLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMWLPQCYRQQRVSKTKTDNNNSNFT 300
DB 443 LYYLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMWLPQCYRQQRVSKTKTDNNNSNFT 502
QY 301 WTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMGCVMIFGKESAGASNTALDNVMTD 360
DB 503 WTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMGCVMIFGKESAGASNTALDNVMTD 562
QY 361 EBEIKATNPVATERFGTYAVNVFQSSSTDPATGDIHAMGALPGMWQDRDVTYLOGPIMAKI 420
DB 563 EBEIKATNPVATERFGTYAVNVFQSSSTDPATGDIHAMGALPGMWQDRDVTYLOGPIMAKI 622
QY 421 PHTDGHFSPPLMGFGGLKNPPOLLIKNTVPANPAPAFSATKFASTFYQSTGQVSE 480
DB 623 PHTDGHFSPPLMGFGGLKNPPOLLIKNTVPANPAPAFSATKFASTFYQSTGQVSE 682
QY 481 IEMELQKNSKRWNPVEQYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534
DB 683 IEMELQKNSKRWNPVEQYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 736

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RESULT 14

```

AD227007
ID AD227007 standard; protein; 736 AA.
XX
AC AD227007;
XX
DT 30-JUN-2005 (first entry)
XX
DE Adeno-associated virus protein SEQ ID NO 157.
XX
KM rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes;
XX scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV;
XX bacterial infection; cancer; ulcerative colitis; antithymatic;
XX antidiabetic; neuroprotective; antiinflammatory; antidiabetic;
XX antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
XX virucide; antibacterial; cytostatic; antitumor; dermatological.
XX
OS Adeno-associated virus.
XX
XX WO2005033321-A2.
XX
PD 14-APR-2005.
XX
PF 30-SEP-2004; 2004MO-US028817.
XX
PR 30-SEP-2003; 2003US-0508226P.
XX
PR 29-APR-2004; 2004US-0566546P.
XX
XX (UYPR-) UNITV PENNSYLVANIA.
XX
XX Wilson JM, Gao G, Alvira MR, Vandenbergh LH;
XX
XX WPI; 2005-285437/29.
XX
PT New adeno-associated virus (AAV) clade comprising at least three AAV
XX members, useful for preventing and/or treating arthritis, multiple
XX sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
XX infection and cancer.
XX
XX Claim 19; SEQ ID NO 157; 569pp; English.

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XX The invention relates to an adeno-associated virus (AAV) clade comprising
CC at least three AAV members, where each member of the AAV clade is
CC phylogenetically related as determined using a Neighbor-Joining heuristic
CC by a bootstrap value of at least 75 % per 1000 isolates and a Poisson
CC correction distance measurement of no more than 0.05. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of rheumatoid arthritis, multiple sclerosis,
CC sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's
CC disease, hemophilia, HIV, bacterial infection, cancer and ulcerative
CC colitis. The present sequence represents the amino acid sequence of an
CC adeno-associated virus protein.

```

Sequence 736 AA:

```

Query Match 99.3%; Score 2885; DB 9; Length 736;
Best Local Similarity 99.1%; Pred. No. 7.5e-234;
Matches 529; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 MASGGA PMADNNGADGVNASGNWCHDSITWLDGRVITTSRTMALPTYNHLYKOISS 60
DB 203 MASGGA PMADNNGADGVNASGNWCHDSITWLDGRVITTSRTMALPTYNHLYKOISS 262
QY 61 ASTGASNDNHFGYSTPWGYDFPNRFCHFSRPRDQRLINNNGFRPKRLNFKLFINIQVK 120
DB 263 TSTGASNDNHFGYSTPWGYDFPNRFCHFSRPRDQRLINNNGFRPKRLNFKLFINIQVK 322
QY 121 EYTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHQGLPPRPADVFMIPQGYLTILN 180
DB 323 EYTTNDGYTTIANNLSTVQVFSDEYQLPYVLGSAHQGLPPRPADVFMIPQGYLTILN 382
QY 181 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSYTFEEVPHSSVYHSSQSLDRLMPLIDQY 240
DB 383 NGSQAVGRSSFYCLEYFSPQMLRTGNFTFSYTFEEVPHSSVYHSSQSLDRLMPLIDQY 442
QY 241 LYYLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMWLPQCYRQQRVSKTKTDNNNSNFT 300
DB 443 LYYLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMWLPQCYRQQRVSKTKTDNNNSNFT 502
QY 301 WTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMGCVMIFGKESAGASNTALDNVMTD 360
DB 503 WTGASKYVNLNGRESIINPGTAMASHKDEDEKFFPMGCVMIFGKESAGASNTALDNVMTD 562
QY 361 EBEIKATNPVATERFGTYAVNVFQSSSTDPATGDIHAMGALPGMWQDRDVTYLOGPIMAKI 420
DB 563 EBEIKATNPVATERFGTYAVNVFQSSSTDPATGDIHAMGALPGMWQDRDVTYLOGPIMAKI 622
QY 421 PHTDGHFSPPLMGFGGLKNPPOLLIKNTVPANPAPAFSATKFASTFYQSTGQVSE 480
DB 623 PHTDGHFSPPLMGFGGLKNPPOLLIKNTVPANPAPAFSATKFASTFYQSTGQVSE 682
QY 481 IEMELQKNSKRWNPVEQYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534
DB 683 IEMELQKNSKRWNPVEQYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 736

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RESULT 15

```

AAB59847
ID AAB59847 standard; protein; 736 AA.
XX
AC AAB59847;
XX
DT 28-MAR-2001 (first entry)
XX
DE AAV6 capsid protein VPI.
XX
XX AAV6: gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;
XX atherosclerosis; sickle cell anemia; thalassemia;
XX blood clotting disorder; diabetes; capsid protein VPI.
XX
OS Adeno associated virus.
XX
XX US6156303-A.

```

Job time : 97.4286 secs

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XX 05-DEC-2000.
PD 11-JUN-1997; 97US-00873168.
XX 11-JUN-1997; 97US-00873168.
XX 11-JUN-1997; 97US-00873168.
XX (UNITW ) UNITV WASHINGTON.
XX PA
XX PI
XX Ruseell DW, Rutledge EA;
XX WPI; 2001-060164/07.
XX
XX Adeno-associated virus serotype 6 and viral vector derived from it for
XX PT gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
XX PT syndrome, sickle cell anemia, thalassemia and diabetes.
XX
XX PS Disclosure; Fig 2; 50pp; English.
XX
XX CC The present invention relates to adeno-associated virus serotypes. The
XX CC present sequence is capsid protein VP1 of one such serotype (AAV6). AAV6
XX CC can be used to construct AAV viral vectors for use in gene therapy for a
XX CC range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,
XX CC sickle cell anaemia, thalassemia, blood clotting disorders and diabetes.
XX CC The AAV viral vectors have increased transduction efficiency of a
XX CC particular host cell as the AAV virion containing the AAV vector genome
XX CC can be modified to express a capsid protein of an AAV serotype that
XX CC transduces the selected host cell
XX
XX SQ Sequence 736 AA;

```

Query Match 99.2%; Score 2884; DB 4; Length 736;
 Best Local Similarity 99.1%; Pred. No. 9.1e-234;
 Matches 529; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MASGGAPMADNNEGADGVCNAGNHCDSITWLGDRVITTTSTRTWALPTYNNHLYKQISS 60
DB 203 MASGGAPMADNNEGADGVCNAGNHCDSITWLGDRVITTTSTRTWALPTYNNHLYKQISS 262
QY 61 ASTGASNDNHYPGYSTPMWGFDFNRFCHFSPRDMORLIINNMGFRPKRLNFKLFNIQYK 120
DB 263 ASTGASNDNHYPGYSTPMWGFDFNRFCHFSPRDMORLIINNMGFRPKRLNFKLFNIQYK 332
QY 121 EVTTNDGVTTIANNLITSTVOVFSDESEYQLPYVLSAHQGLPPPADVFMIPOYGYLTIN 180
DB 323 EVTTNDGVTTIANNLITSTVOVFSDESEYQLPYVLSAHQGLPPPADVFMIPOYGYLTIN 382
QY 181 NSQAVGRSSFCLEYPFSQMLRTGNNFTFSYTFEEVPHHSYAHQSGLDRLNPLIDQY 240
DB 383 NSQAVGRSSFCLEYPFSQMLRTGNNFTFSYTFEEVPHHSYAHQSGLDRLNPLIDQY 442
QY 241 LYYLNTNONGSAGNNDLLFSRGSPPAGMSVOPKNNLPGPCYRQORVSKTKTDNNSNFT 300
DB 443 LYYLNTNONGSAGNNDLLFSRGSPPAGMSVOPKNNLPGPCYRQORVSKTKTDNNSNFT 502
QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASNTALDNWMTD 360
DB 503 WTGASKYNLNGRESIINPGTAMASHKDEKDXKFFPMGCVMI FGKESAGASNTALDNWMTD 562
QY 361 EEEIKATNPVATERFGTVAVNFOSSSTDPATGVDHAMGALPGMWODRDVYLGQPIWAKI 420
DB 563 EEEIKATNPVATERFGTVAVNFOSSSTDPATGVDHAMGALPGMWODRDVYLGQPIWAKI 622
QY 421 PHTDGHFSPPLMGFGFLKNPPQIILIKNTVPVNPANPPAEPASATKFAFITQYSTGVSV 480
DB 623 PHTDGHFSPPLMGFGFLKNPPQIILIKNTVPVNPANPPAEPASATKFAFITQYSTGVSV 682
QY 481 IEMELQKNSKRNNPEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB 683 IEMELQKNSKRNNPEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2005, 17:29:19 ; Search time 18.8571 Seconds
(without alignments)
2724.684 Million cell updates/sec

Title: US-10-696-282-17

Sequence: 1 MASGGAPMADNNEGADGVG.....NNGLYTEPRPIGTRYLTPL 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2177.5	74.9	504	1 VCPV3A	coat protein - ade
2	1676	57.7	732	2 S52210	coat protein VP1 -
3	517	17.8	673	1 VCPVB5	coat protein VP1 -
4	487.5	16.8	781	1 VCPV19	coat protein VP1 -
5	234.5	8.1	723	1 VCPVBP	coat protein VP1 -
6	232.5	8.0	729	1 A60006	coat protein VP1 -
7	232.5	8.0	729	1 VCPVNA	coat protein VP1 -
8	229	7.9	587	1 B44276	coat protein VP1 -
9	226	7.8	722	1 VCPV2	coat protein VP1 -
10	197	6.8	716	1 VCPV2M	coat protein VP1 -
11	196.5	6.8	718	1 VCPVIM	coat protein VP1 -
12	194	6.7	722	1 VCPVME	coat protein VP1 -
13	194	6.7	727	1 VCPVIF	coat protein VP1 -
14	189	6.5	584	2 S49594	capsid protein VP2
15	189	6.5	727	1 VCPVFP	coat protein VP1 -
16	188	6.5	737	1 VCPVCD	coat protein VP1 -
17	184	6.3	748	1 VCPVCP	coat protein VP1 -
18	177.5	6.1	702	1 VCPVAP	coat protein VP1 -
19	175	6.0	722	1 VCPVCN	coat protein VP1 -
20	123.5	4.2	680	2 AB0124	probable TonB-depe
21	122.5	4.2	880	1 SYBSVS	valine-RNA ligase
22	121	4.1	635	2 P96660	protein FZK1.10
23	118	4.1	739	2 T52289	probable transketo
24	115.5	4.0	345	1 B97024	probable phosphoe
25	113.5	3.9	2817	2 B97033	uncharacterized pr
26	109	3.8	1072	2 T35753	probable periplasm
27	109	3.8	1072	2 A86827	hypothetical prote
28	109	3.8	1186	2 T18210	delta endotoxin -
29	108.5	3.7	1711	2 AB1283	peptidoglycan link

30	108	3.7	655	1 ALKRG	cyclomaldextrin
31	108	3.7	772	1 A44052	outer layer protei
32	108	3.7	826	2 AD1683	penicillin-binding
33	107.5	3.7	413	2 T23098	hypothetical prote
34	107.5	3.7	648	2 S50856	whn protein - rat
35	107	3.7	777	2 AE0462	probable exported
36	107	3.7	1338	2 T30565	MAP kinase kinase
37	106.5	3.7	403	2 B87513	acyl-CoA dehydroge
38	106	3.6	1271	2 D64237	hypothetical prote
39	105.5	3.6	2500	2 G71609	hypothetical prote
40	105	3.6	1394	2 A29637	position-specific
41	104.5	3.6	559	2 S33724	transcription fact
42	104.5	3.6	717	2 H85171	DEF (CIA1) protein
43	104	3.6	395	2 S50966	MAR1 protein - yea
44	104	3.6	715	2 H90977	hypothetical prote
45	104	3.6	719	2 F85824	hypothetical prote

ALIGNMENTS

RESULT 1

VCPV3A

coat protein - adeno-associated virus type 2

C:Species: adeno-associated virus type 2

C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004

C:Accession: A03698

R:Srivastava, A.; Lusby, E.W.; Berns, K.I.

J. Virol. 45, 555-564, 1983

A:Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome.

A:Reference number: A03694; PMID:83164299; PMID:6300419

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-504 <SRI>

A:Cross-references: UNIPROT:P03135; UNIPARC:UPI0000127C8E; EMBL:J01901; NID:G209616; PDB

C:Superfamily: adeno-associated virus coat protein

C:Keywords: coat protein

Query Match 74.9%; Score 2177.5; DB 1; Length 504;
Best Local Similarity 82.5%; Pred. No. 1.4e-152;
Matches 392; Conservative 33; Mismatches 47; Indels 3; Gaps 2;

QY	1	MASGGAPMADNNEGADGVGNAAGWCHDSTWLGDRVITTTSTRTALPTNNHLYKQISS	60
DB	1	MATGSGAPMADNNEGADGVGNSGWHCDSTWMDRVTITSTRWALPTNNHLYKQISS	60
QY	61	ASTGASNDNHYRGYSTPMGYPDPNRFCHFSFRDMORLNNWGRPRKLNFKLFNIQVK	120
DB	61	QS-GASNDNHYRGYSTPMGYPDPNRFCHFSFRDMORLNNWGRPRKLNFKLFNIQVK	119
QY	121	EYTTNDGVTITANNLTSTVQFSDSEYOLPYVLGSAHQCLPPPADVEMIDQYGLTLN	180
DB	120	EYTTNDGVTITANNLTSTVQFSDSEYOLPYVLGSAHQCLPPPADVEMIDQYGLTLN	179
QY	181	NSQAVGRSSFYCLEYFESQMLRTGNFTFSTFEBVPPHSSVYASQSLDRMLNPLIDY	240
DB	180	NSQAVGRSSFYCLEYFESQMLRTGNFTFSTFEBVPPHSSVYASQSLDRMLNPLIDY	239
QY	241	LYVLRNTQNSGSAQKDLFSRGSFAGMSVCPKMWLPQPCROORVSKTKTDNNNSFT	300
DB	240	LYVLRNTQNSGSAQKDLFSRGSFAGMSVCPKMWLPQPCROORVSKTKTDNNNSFT	299
QY	301	WTGASKYNNLNGRESIIPGTAMASHKDDKFFPMGSMVIFPKESAGSNTALDNVMTD	360
DB	300	WTGATKYNLNGRDSLVP--AMASHKDDKFFPMGSMVIFPKESAGSNTALDNVMTD	357
QY	361	EEBIRKATNPATERTCTVAVNFQSSSTDPATGDAHMGALPGMWODRVPYIQGPYIWKI	420
DB	358	EEBIRKATNPATERTCTVAVNFQSSSTDPATGDAHMGALPGMWODRVPYIQGPYIWKI	417
QY	421	PHTDGHFHSPLMGSGGLKMPPOILIKTTPVAPNPAFSAATKFASTFYOSTG	475
DB	421	PHTDGHFHSPLMGSGGLKMPPOILIKTTPVAPNPAFSAATKFASTFYOSTG	475

Db 418 PHTDGHFHPSPLMGGFGLKHPPOILIKNTVPANPSTTFSNAKPFASFIOTYSTG 472

RESULT 2

S52210

coat protein VP1 - muscovy duck parvovirus

N/Alternate names: VP1 protein

C/Species: muscovy duck parvovirus

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S52210

R/Zadori, Z.; Ederl, J.; Nagy, J.; Kisari, J.

Submitted to the EMBL Data Library, September 1993

A/Reference number: S52209

A/Accession: S52210

A/Molecule type: DNA

A/Residues: 1-732 <ZAD>

A/Cross-References: UNIPROT:Q83289; UNIPARC:UPI000006C6SD; EMBL:X75093; NID:G609091; PID

A/Experimental source: strain FM

C/Genetics:

A/Gene: VP1

C/Superfamily: parvovirus coat protein

C/Keywords: coat protein

Query Match 57.7%; Score 1676; DB 2; Length 732;

Best Local Similarity 56.9%; Pred. No. 2,1e-115;

Matches 308; Conservative 77; Mismatches 142; Indels 14; Gaps 6;

QY 1 MASGGAPMADNNEGADGVGNASGNMHCSTMLGDRVITTSRTWALPFTYNNHLYKOISS 60

Db 199 MABGGAGAGDAGAGADGVGNASGNMHCSTMLGDRVITTSRTWALPFTYNNHLYKOISS 258

QY 61 ASTGASNDNHVFGYSTPMGYPDFNRFCHFSRPRDQRLINNMGFRPKLNFVKI 120

Db 259 GINPDSN-TQVAGYSTPMGYPDFNRFCHFSRPRDQRLINNMGFRPKLNFVKI 317

QY 121 EYTTNDGVTTIANMLTSTVQVFSDBSYQLPYVLGSAHQGLRPPADVFMIPOYGYLTN 180

Db 318 EYTTDQDTKIANNLTSTIQITFDNEHQLPYVLGSAHQGLRPPADVFMIPOYGYCTMH 377

QY 181 ---NSQAVGRSSFCLEFFPSOMLRTGNFTFSYTFEEVPHSSVYASQSLDRIMNLI 237

Db 378 TNQSGARFENDRAFYCLEFFPSOMLRTGNFTFSYTFEEVPHSSVYASQSLDRIMNLI 437

QY 238 DQYLYLNRTQNSGSAQNKDLLFSRGPAGMSVOPKMWLPGPCYRQORVSKTK--TDNN 295

Db 438 DQYLYNFSFV-NGGNAAQ-----FKAVYGAAGANGRMWLPSPKLLDQRYRAYSGCTNY 491

QY 236 NSNFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMSCVMTFGKE--SAGASNTAL 353

Db 492 ANMSIMSKGNKVFLEKDRYLQPGVATHTHEDQASSVPAQNIIGIAKDPYRSGSTLAGI 551

QY 354 DNVMITDEBEIKATNPVATERFGYAVVNROSSSTPATCDVHAMALPGMWQDDVYLQ 413

Db 552 SIIWYTDDEIAPLPTNGVGRPYGLTVTNQNTTAPVNALEVLALPQMWQNDIYLQ 611

QY 414 GPIMAKIPTDGHFHPSPLMGGFGLKHPPOILIKNTVPANPAPAEFATKPFASFIOTYS 473

Db 612 GPIMAKIPTDGHFHPSPLMGGFGLKHPPOILIKNTVPADPRLPDEVYVQKNKSTIOTYS 671

QY 474 TQGVSEIEMELOKENSKRANPEVOYTSNYAKSANDFTVNNGLYTEPRPIGTRYLTRP 533

Db 672 TQGVSEIEMELOKENSKRANPEVOYTSNYAKSANDFTVNNGLYTEPRPIGTRYLTRP 731

QY 534 L 534

Db 732 L 732

RESULT 3

VCPVBS

coat protein VP1 - bovine parvovirus

N/Contains: coat protein VP2

C/Species: bovine parvovirus

C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: A26104

R/Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.; Bates, R.C.

J. Virol. 60, 1085-1097, 1986

A/Title: Complete nucleotide sequence and genome organization of bovine parvovirus.

A/Reference number: A26104; MUID:87061184; PMID:3783814

A/Accession: A26104

A/Molecule type: DNA

A/Residues: 1-673 <CHB>

A/Cross-References: UNIPROT:P07297; UNIPARC:UPI0000127D77; EMBL:M14363; NID:G333454; PID

C/Superfamily: parvovirus coat protein

C/Keywords: coat protein

F/138-673/Product: coat protein VP2 #status predicted <VP2>

Query Match 17.8%; Score 517; DB 1; Length 673;

Best Local Similarity 25.1%; Pred. No. 4.4e-30;

Matches 143; Conservative 85; Mismatches 208; Indels 134; Gaps 17;

QY 5 GGAPMADNNEGADGVGNASGNMHCSTMLGDRVITTSRTWALPFTYNNHLYKOISSASTG 64

Db 163 GSGSVGGGRGSGSVGVTGQMTGTIFSENIYVTKNTROPICDKGHLYKS-EVLNTG 221

QY 65 ASNDNHVFGYSTPMGYPDFNRFCHFSRPRDQRLINNMGFRPKLNFVKI 124

Db 222 DTAHRY-ATTPSYNFMQYSSHFSRPNQHLVNDYERRPRAMTVRYNLIQKIMT 280

QY 125 NDGVTTIAN-LTSTVQVFSDBSYQLPYVLGSAHQGLRPPADVFMIPOYGYLTN 179

Db 281 DGAMGYTNNDLTGMHIFCDGHRIRYVQHPMDQCMPELPSNIMELPOYAYIPAPISV 340

QY 180 ---NSQAVGRSSFCLEFFPSOMLRTGNFTFSYTFEEVPHSSVYASQSLDRIL 232

Db 341 VDNNTTWTVEHLLKGVPLVLENSDHEVLANG-----RI 375

QY 233 MNPILDQYLYLNRTQ-----OSGSAQNKDLLFSRGP-----AGMSVOPKMWL 277

Db 376 YRIYIOLMRLEMDRKHQIHASDVOSTGQKQNLIIQKQPNKORFONAAALRTISM 435

QY 278 PGPCYRQORVSKTKDNNNSFTWTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMSC 337

Db 436 SGP-----GIARGHNAITLQTSAGALVTWNTGAD-----VSG 469

QY 338 VM-----IFGKE-----SAGASNTALDNVMTDEBEIKATNPVAT 372

Db 470 VRAVVGYSTPIVGGQPSDDLRLRYASAAAGQNPILN-----AAR 515

QY 373 ERFGTVAVNFOSSSTPATGCVHAMALPGMWQDDVYLQGPIMAKIPTDGHFHPSP 432

Db 516 HTFTRERATKLIITSGNADGQYKEMWLPMQWMSAPISRYNPIMVAVPRVNRKTLTLDQ 575

QY 433 MGGFGLKHPPOILIK--NTPVPANPAPAEFATKPFASFIOTYSTGOVSEIEMELOKENS 490

Db 576 DGSIFMGSHPPTIYIKLARIYVPGND-----SFLNYYTVQGVSCVAVWEVERKGT 626

QY 491 KRANPEVOYTSNYAKSAND-FTVNNGLY 519

Db 627 KNMRPEYVHS--ATNMSVDAYTINNAGVY 653

RESULT 4

VCPV19

coat protein VP1 - parvovirus B19 (strain Au)

C/Species: parvovirus B19

A/Note: host Homo sapiens (man)

C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: A24299

R/Shade, R.O.; Blundell, M.C.; Colmore, S.F.; Tattersall, P.; Astell, C.R.

J. Virol. 58, 921-936, 1986

A/Title: Nucleotide sequence and genome organization of human parvovirus B19 isolated from

A/Reference number: A24299; MUID:86200451; PMID:3701931

A/Accession: A24299

A/Molecule type: DNA

A/Residues: 1-781 <SHA>

A:Cross-references: UNIPROT:P07299; UNIPARC:UP10000127D7C; EMBL:M13178; NID:g333375; PIR
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 16.8%; Score 487.5; DB 1; Length 781;

Best Local Similarity 27.4%; Pred. No. 8.3e-28;

Matches 143; Conservative 84; Mismatches 239; Indels 55; Gaps 16;

QY 10 ANNNEGADGVGNAS--GNMHCDSTWLGDRVITTTSTRTMALPTYNNHLYKQISSASTGASN 67
DB 234 AASASTGAGGGSNSVSKMSSEKATFSANVTCTFSQFLIPYDPEHHYKVFSPASASCHN 293
QY 68 D-----NHFGYSTPMGYFDNRHCHSPDMDQRLINNMGFRKALNFTLPMI 117
DB 294 ASGKAQVCTISPIFMGYSTPMRYLDENALNLFPSFLFQHLIENGYISAPDALVTYISBI 353
QY 118 QYKEVLT--TNDGVTTIANNLTSTVOVFSDESEYOLPVLGSAHQGLPPPADVFMPOG 175
DB 354 AVKDVTDKTGAGV-QVTDSTGRLCMLVDEHYKPYVLGQGDPTLAPELPIVYPPPOYA 412
QY 176 YLTLAN-GSQAVG-----RSSFYCLEYFPPSQMLRTGNNTFSYTEEVPFSSYAH 225
DB 413 YLTGVVNTQGISGDSKSLASESAFYVLEHSSFOLLGTGTAASMKYKFPVPEMLBEG 472
QY 226 SQGLDLRLMPLIDVLYLNTQNGSAQNKDLFSRGSAPAGMSVQPKMLPGCYRQO 285
DB 473 SQHFEMYNPL---YGSRLGVDPDTLGDPEKFRSL-----THBDHALQPNFMFGPLVNSV 524
QY 286 RUSKTTDNNNSFTWTGASKYLNGLRESIINRG-TAMASHKDEKFFPMGCVMLFGKE 344
DB 525 STKEGSSVTGAKKALTLGISTGSTRISLSPGPNVSPQYHMDTKYTGAINAISHQOT 584
QY 345 SAGASATLADNV-----MITDEEIKATNPVATERFGTVAVNFOSSSTDPATGDNAM 397
DB 585 TYG---NAEKKEVQGVGRPRNEKQKQGLAMHTY-----FNGKGTQVTDQIE-R 634
QY 398 GALPGWVODRDVYLOGPIWAKIPHTDGHFHS-PLMGFGELKNPPQILLKNTPYPANP 456
DB 635 PLWVGSVNMRRAHYESQLSKIPNLDDSFKQFALGGGHLHQPPOIFLK--ILPQSG 692
QY 457 PAEFSATKPAFTTOYSTGVSVIEML-QKNSKRWNP 496
DB 693 PIGIKSMGITTLVQYAVGIMTVMTFKLPKPRKATGKRMNQ 733

RESULT 5

VCPPVP

coat protein VP1 - porcine parvovirus

N:Contains: coat protein VP2

C:Species: porcine parvovirus

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

R:Ranz, A.I.; Mancius, J.U.; Diaz-Aroca, E.; Casael, J.I.

J. Gen. Virol. 70, 2541-2553, 1989

A:Title: Porcine parvovirus: DNA sequence and genome organization.

A:Reference number: A33302; MUID:90010964; PMID:2794971

A:Accession: B33302

A:Molecule type: DNA

A:Residues: 1-723 <RAN>

A:Cross-references: UNIPROT:P18546; UNIPARC:UP10000174964; EMBL:D00623

C:Genetics:

A:Initons: 10/1

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein
F,145-723/Product: coat protein VP2 #status predicted <VP2>

Query Match 8.1%; Score 234.5; DB 1; Length 723;

Best Local Similarity 23.2%; Pred. No. 3.2e-09;

Matches 139; Conservative 83; Mismatches 241; Indels 137; Gaps 32;

QY 3 SGGGAPMADNNEGADGVGNASGNMH--CDSTWLG---RVITTSRTMALPTYNNHLYKQ 57
DB 168 SGGGGG-GGGGAGAGVGVSTGSPNNQTFQYLDEGLVRIITAHASRLIHLNMBEHETTKR 226

QY 58 I-----SSASTGAS-NDNHFGYSTPMGYFDNRHCHSPDMDQRLINNMGFRKRLN 111
DB 227 IHLNSESAGAGVQVODAHQMTWMLIDANAKGFNPADQILNNMTEINLVSE 286

QY 112 FKLPMIQKEVLT--TNDGVTTIANNLTSTVOVFSDESEYOLPVLGSAHQGLPPPADV 168
DB 287 QALFNVVLTITESTATSPPTKIYNNDLTASLMVLDNTNLTLPYTPAARSETLGFYPLP 346

QY 169 FMIPQGYL-----TLNNSQAVGRSS-----FYCLE-YFPPQMLRTGNKF 208
DB 347 TKPTQRYYLSCIRMLNPPYTGQSQPNRNRLNTHSDIMEYTTIENAVPIHLTGTGEF 406

QY 209 -TFSTFEVPPHSSYASQSILR-----LNNPL--DOYLYLARTQNGSAQNK 257
DB 407 STGIYHFDTKPL--KLTHSWQTRSLGLPKLITETTEGDQPGTLPAANTKRYHOTI 464

QY 258 DLLFSGSPAGMSVQPKMLPGCYRQORVSKTKDNNNSFTWTGASKYLNGLRESIIN 317
DB 465 NNSYTEAT---AIRP-----AQGVNTPYMNFYENGGRF-----LT 498

QY 318 P--GTAMASHKDEDEKFFPMGCVMLFGKSAGASTALD--NVMITDEEIK--ATNP- 369
DB 499 PIVPTADQYNDDEPN-----GAIRFTMDYQHGLTTSQELERYTFPNQ 543

QY 370 ----VATERGTV-VNFOSS-----TDPATG--DVHAMGALP-----GMWQDRV 410
DB 544 SKCGRAPKQFNOQAFLNLENTNGLTLPSPDIEGKSNMHEFNNTLTYGRLTALNNTAV 603

QY 411 YLOGPIWAKIPHTD--GHFPEPLMGFGELK-NPPQILLKNTPYPANPPEFSA-TKPA 466
DB 604 FNGQIMDKELDTLKPRLH--VTAFFCKKNPPQGLFVKIAP--NLTDFFNDSPOQ 657

QY 467 SEITQYSTQGVSVIEMLQKNSKRWNPDEVQYTSNYAKSANVDFTVNNGLYTEBRPIG 526
DB 658 PRLITYSNFMKGLTLFTAKKSSNMWNPICQHTT-----TAENIGHYI-PTNIG 706

RESULT 6

A60006

coat protein VP1 - porcine parvovirus (strain 90HS)

N:Contains: coat protein VP2

C:Species: porcine parvovirus

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: A60006

R:Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.

Virus Res. 13, 79-86, 1989

A:Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.

A:Reference number: A60006; MUID:89319168; PMID:2750278

A:Accession: A60006

A:Molecule type: DNA

A:Residues: 1-729 <SAK>

A:Cross-references: UNIPROT:P33484; UNIPARC:UP10000127C6E

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein; glycoprotein

F,151-729/Product: coat protein VP2 #status predicted <VP2>

F,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #stact

Query Match 8.0%; Score 232.5; DB 1; Length 729;

Best Local Similarity 23.0%; Pred. No. 4.5e-09;

Matches 137; Conservative 86; Mismatches 245; Indels 127; Gaps 31;

QY 3 SGGGAPMADNNEGADGVGNASGNMH--CDSTWLG---RVITTSRTMALPTYNNHLYKQ 57
DB 174 SGGGGG-GGGGAGAGVGVSTGSPNNQTFQYLDEGLVRIITAHASRLIHLNMBEHETTKR 232
QY 58 IS--SASTGAS---NDNHFGYSTPMGYFDNRHCHSPDMDQRLINNMGFRKRLN 111
DB 233 IHLNSESAGAGVQVODAHQMTWMLIDANAKGFNPADQILNNMTEINLVSE 292
QY 112 FKLPMIQKEVLT--TNDGVTTIANNLTSTVOVFSDESEYOLPVLGSAHQGLPPPADV 168
DB 293 QELFNVVLTITESTATSPPTKIYNNDLTASLMVLDNTNLTLPYTPAARSETLGFYPLP 352

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QY 169 FMIPQGYL-----TLNNGSAVGRS-----SFYCLE-YFPGMLRTGNNF 208
D 353 TKPQYRYVLLSCTRLNLPPTTGGSOQITDSIQGLHSDIMFYTIENAVPIHLRTGDEF 412
QY 209 -TFSYTFEEVPHSSVYASQSLDR-----LMNPIL--DOYLYLNRTONOGSQAOK 257
D 413 STGIYHFDTPRL--KLTHSQWTRSLGLPRKLLTEPTBEDQHPGTLPAANTRKGYHQT 470
QY 258 DLFSRGPSPAGMSVOPKRWLPGPCYRQORVSKTIDNNNSNFTWGAASKYNLNGRESIIN 317
D 471 NNSYTEAT--AIRP-----AQGVNTPYNNFEYSNGGPF-----LT 504
QY 318 P--GTAMASHKDEDEKFFPMGSMIFGKESAGASNTALDNVMTDEBEIKATNP----- 369
D 505 PIVFPAADQYNDDE-----PNGAIRFTMGYQHGLTTS-----SGELERYTFNPQSKGR 554
QY 370 VATERFGTYA-VNFOSSS-----TDPATG--DVHAMGALP-----GMVMQDRDYVLOGP 415
D 555 APKQGFNOQAPLNLNTNNGTLLPSPDPIGSKNMFMTTLNTYGLTLALNTAPVFPNGQ 614
QY 416 IMAKIPIHND--GHFSPPLMGFGGLK--NPPQILIKNTPVANPPAEFSA--TKFASFTQ 471
D 615 IWDKELDLDLTKRRLH---VTAPFVCKNPPQGLPFVKIAP---NLTDFFNADSPQGPRIIT 668
QY 472 YSTGVSVSEIEMELQKENSKRNNPEVOYTSNAYKASANDFTVDNGLYTEPPPIG 526
D 669 YSNFMWKGLTFTAKRSMNMNPIQOHTT-----TANIGNYI-PTNIG 712
```

RESULT 7
VCPVNA
coat protein VP1 - porcine parvovirus (strain NADL-2)

N.Contains: coat protein VP2
C.Species: porcine parvovirus
C.Date: 31-Dec-1990 #sequence__revision 31-Dec-1990 #text_change 09-Jul-2004
C.Accession: B33743; D48472
R.Vasudevaraya, U.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 173, 368-377, 1989
A.Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal pe
A.Reference number: A33743; MUID:90085785; PMID:2596019
A.Molecule type: DNA
A.Residues: 1-729 <VAS>
A.Cross-references: UNIPROT:P18546; UNIPARC:UPI0000127C70; GB:M32787; NID:G332983; PIDN:
R.Bergeron, U.; Menezes, U.; Tjissen, P.
Virology 197, 86-98, 1993
A.Title: Genomic organization and mapping of transcription and translation products of p
A.Reference number: A48472; MUID:94025614; PMID:8212598
A.Accession: D48472
A.Molecule type: DNA
A.Residues: 11-729 <BER>
A.Cross-references: UNIPARC:UPI0000174965
A.Experimental source: NADL-2, ATCC VR-742
A.Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBI:P138794)
C.Genetics:
A.Introns: 10/1
C.Superfamily: parvovirus coat protein
C.Keywords: coat protein; glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 8 0%; Score 232.5; DB 1; Length 729;
Best Local Similarity 23.0%; Pred. No. 4,5e-09;
Matches 138; Conservative 85; Mismatches 240; Indels 137; Gaps 32;

```
QY 3 SGGGAPMADNNEGADGVNAGS--NMHCDSTWIGD---RVITTSRTMALPTYNHLYKO 57
D 174 SGGGGG--GGGGAGAGVGSTGTGNNQTEFOYLGISGLVAVITAHASRLHLNLPHEIETKR 232
QY 58 IS--SASTGAS---NDNHYFGYSTPWGYFDNRFCHSPSPDMQRLINNMGFPKRLN 111
D 233 IHLNSESAGVAGMVDDAHQTQVTPWLSLDANAMGVWENPADWQLISNNMTEINLVSE 292
```

```
QY 112 FKLNIQVKEVT---TNDGYTTIANNLSTVQVFSDEYOLPYVLGSAHQCCPPPADV 168
D 293 QELFNVLKTIITSATSPPPKIYNNDLTAISLVALDTNNLTLPYTPAAPRSSETLGFPYMLP 352
QY 169 FMIPQGYL-----TLNNGSAVGRS-----SFYCLE-YFPGMLRTGNNF 208
D 353 TKPQYRYVLLSCTRLNLPPTTGGSOQITDSIQGLHSDIMFYTIENAVPIHLRTGDEF 412
QY 209 -TFSYTFEEVPHSSVYASQSLDR-----LMNPIL--DOYLYLNRTONOGSQAOK 257
D 413 STGIYHFDTPRL--KLTHSQWTRSLGLPRKLLTEPTBEDQHPGTLPAANTRKGYHQT 470
QY 258 DLFSRGPSPAGMSVOPKRWLPGPCYRQORVSKTIDNNNSNFTWGAASKYNLNGRESIIN 317
D 471 NNSYTEAT--AIRP-----AQGVNTPYNNFEYSNGGPF-----LT 504
QY 318 P--GTAMASHKDEDEKFFPMGSMIFGKESAGASNTALD--NVMTDEBEIK--ATNP- 369
D 505 PIVFPAADQYNDDEPN-----GAIPTMDYQHGLTTSQGLERYTFNFPQ 549
QY 370 ---VATERFGTYA-VNFOSSS-----TDPATG--DVHAMGALP-----GMVMQDRDY 410
D 550 SKCGRAPKQGFNOQAPLNLNTNNGTLLPSPDPIGSKNMFMTTLNTYGLTLALNTAPV 609
QY 411 YLOGPIWAKIPIHND--GHFSPPLMGFGGLK--NPPQILIKNTPVANPPAEFSA--TKFA 466
D 610 PPNQIWDKLDLDTLTKRRLH---VTAPFVCKNPPQGLPFVKIAP---NLTDFFNADSPQ 663
QY 467 SFTQYSTGVSVSEIEMELQKENSKRNNPEVOYTSNAYKASANDFTVDNGLYTEPPPIG 526
D 664 PRITTSNFMWKGLTFTAKRSMNMNPIQOHTT-----TANIGNYI-PTNIG 712
```

RESULT 8

coat protein VP1 - parvovirus Iu111
C.Species: parvovirus Iu111
C.Date: 17-Feb-1994 #sequence__revision 17-Feb-1994 #text_change 09-Jul-2004
C.Accession: B44276
R.Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederman, M.
Virology 192, 339-345, 1993
A.Title: The complete nucleotide sequence of parvovirus Iu111 and localization of a unqt
A.Reference number: A44276; MUID:93297126; PMID:8517025
A.Accession: B44276
A.Status: translation not shown
A.Molecule type: DNA
A.Residues: 1-587 <DIF>
A.Cross-references: UNIPROT:P36310; UNIPARC:UPI0000127D7E; GB:M81888
C.Superfamily: parvovirus coat protein
C.Keywords: coat protein; glycoprotein
F:49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 7 9%; Score 229; DB 1; Length 587;
Best Local Similarity 22.7%; Pred. No. 5,9e-09;
Matches 133; Conservative 74; Mismatches 228; Indels 150; Gaps 28;

```
QY 3 SGGGAPMADNNEGADGVNAGS--NMHCDSTWIGD---RVITTSRTMAL--PTYNH--- 52
D 30 SGGG-----GSGGGGAGVGSTGSDNQTGKFLDGWVEITAYSTRVHNLMPSENYCR 83
QY 53 ---HLYKOISASYGANDNHYFGYSTPWGYFDNRFCHSPSPDMQRLINNMGFPKRL 109
D 84 VRVINTNDTGTASIMAMDHAHQIW--TPWGLVDANAMGVWQPSDQYISNNMHIHLHS 142
QY 110 LNFKLNIQVKEVT--TNDGYTTIA--NMLTSYQVFSDEYOLPYVLGSAHQCC--- 161
D 143 LDGELFNVLKTIYEQUTGAELIKYVNNDDLAAAMVVALDSNNILPYTPALDNGELTFYP 202
QY 162 --PEPPA-----DYFMIPQGYLTLNNGSAVGRSSSYCLEYFSS--QMLATGN 206
D 203 WKPTIPSPRYRYFSCDRNLSTYKDEAGTITDNGLASGLNSQPTLENTQRIINLRTGD 262
```


Db 638 YDPNATLISRIYTGTFPFMKGLTRAKLRA-----NTWNPVYQVSAS-----D 682
QY 515 NNGLY---TEPPRIGT-----RYLTRPL 534
Db 683 NGNSYMSVTKMLPTATGNMQSVLITRPV 711

RESULT 11

VCPVIM

coat protein VP1 - minute virus of mice (strain WVM1)

C:Species: minute virus of mice, murine parvovirus

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: B23008; B29510

R:Sahl, R.; McMaster, G.K.; Hilt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A:Title: DNA sequence comparison between two tissue-specific variants of the autonomous

A:Reference number: A23008; MUID:85242059; PMID:3855242

A:Accession: B23008

A:Molecule type: DNA

A:Residues: 1-718 <SAH>

A:Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; NID:g60918; PIDN

R:Abdel, C.R.; Gardiner, E.M.; Tattersall, P.

J. Virol. 57, 656-669, 1986

A:Title: DNA sequence of the lymphotropic variant of minute virus of mice, WVM(1), and C

A:Reference number: A29510; MUID:86115415; PMID:3502703

A:Accession: B29510

A:Molecule type: DNA

A:Residues: 1-143, A, 145-718 <AST>

A:Cross-references: UNIPARC:UPI000127D6C; EMBL:M12032

A:Title: parvovirus coat protein

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein

Query Match 6.8%; Score 196.5; DB 1; Length 718;
Best Local Similarity 20.5%; Pred. No. 26-06;
Matches 122; Conservative 82; Mismatches 243; Indels 147; Gaps 25;

QY 3 SGGGAPMADNNEGADGVNAGSNMHCDS--TWLGD---RVITTSRTNALPTVNNHLLKQ 57
Db 161 SGGG-----GGGGGAGVSTGSDYNQTHYRFLGSGWEITLALRLVHLMKSENYCR 214
QY 58 I-----SSASTGASNDNHVFGYSTPMGYPDFNRFCHFSRPRDWQRLINNMGFRPKRL 110
Db 215 IYVHNTTDSVAKGNMAKDHAHQIWTPMGLVDANMAGVWLQPSDWQYICNTMSQNLVSL 274
QY 111 NKLRLPIQVKEYTTND---GVTTANLITSTVQVFSSEYQLPYVLSAAGCLPPPPA 166
Db 275 DQEIFVVLKTYTEODSGQAIRKYNNDLTACMVAVDVSNMLPYTPAANSMETLGFYFW 334
QY 167 DVFMIPQYGY-----LTLNN-----GSAVGRSSFCLEFFPS-OMLRTGN 206
Db 335 KPTIASPIYFYPCVDRDLSTYENOGTIEHVMGTPKMSQFFIENITQITLIRGCD 394
QY 207 NF-TESYTEEEVFPSSVAHSQSLRLMN--PLIDQVLYLNRTONQSSAQNKLFSR 263
Db 395 EFATGYVYFDTPNV--KLHTWQTNKQLGQPLLSF---PEADTDAGT-----LTAQ 442
QY 264 GSPAGMSVQPKWL-----PGCYRQORVSKTIDNNNSNF 299
Db 443 GSRHGTQMEVNMVWSEAIRTPAQVFCQPHNDFEASRAGP-FAAPKPADVTQGVDBRA 501
QY 300 TWTGASKYMLNGRESIINPGTAMASHKDEDKF-----FPMGVMIPKESAGASN 350
Db 502 NGSVRSYSGKQGENMAAGPAPERITWDETNGSGRDRDGTQISAPLVVPPPLNGILIT 561
QY 351 TALDNVMTDEBEIKATNPATERFGTVANFQS--SSTDPAATGDVHAMGALPGMWODR 408
Db 562 NA-----NPITGN-----DIHFSNVNSYGPLAFSH-----PS 591
QY 409 DYLQGPPIAK---IHTDGHFHSPLMGFGKLPPOILIKNTP--VPANPPAFSAT 463
Db 592 PVPFOQIWDKELDEHKRLHITAPFV--CKNNAFGQMLVRLGPNLTQDYDPNGATLS 648

QY 464 KFASTFOYSTGVSEIEMELOKENSRRNPEVOYTSNYAKSANDPTVDNG 517
Db 649 RIYVYTGTFPFMKGLTRAKLRA-----NTWNPVYQ-----VSVEDNG 686

RESULT 12

VCPVMS

coat protein VP1 - mink enteritis virus (strain Abashiri)

N:Contains: coat protein VP2

C:Species: mink enteritis virus, MEV

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: B38350

R:Katsunari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishiguro, N.; Goto, H.; Shingai,

J. Gen. Virol. 72, 867-875, 1991

A:Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the

A:Reference number: A38350; MUID:9120123; PMID:2016597

A:Accession: B38350

A:Molecule type: DNA

A:Residues: 1-722 <KAR>

A:Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765

C:Superfamily: parvovirus coat protein

C:Keywords: coat protein

F:113-722/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.7%; Score 194; DB 1; Length 722;
Best Local Similarity 20.7%; Pred. No. 3.1e-06;
Matches 136; Conservative 73; Mismatches 215; Indels 232; Gaps 32;

QY 5 CGAPMADNNEGADGVNAGSNMHCDSITLDRVYTTST-----RTNALPTVNN- 52
Db 148 GGGP-AVRNERATSGSGSGGGGGS--GGVSTGTFTNNQTFKFLNGWEITANSS 204
QY 53 ---HL-----YKQI-----SSASTGASNDNHVFGYSTPMGYPDFNRFCHFSRPRDW 95
Db 205 RLVLHNPESSENYKRVVNNMDKTAIVGNMALLDTHQIYTPMSLVDANMAGVWFNPGDW 264
QY 96 QRLINNMGFRPKRLNKLPIQVKEYT---TNDGVTTANLITSTVQVFSSEYQLPYV 152
Db 265 QLIYNTSELHVSFEQDIFVVLKTVSBSATQPTKYVNNDLTASIMVLDNSNTMPFT 324
QY 153 LGSAGGCL-----PPPPA-----DVFMIPQYGYLTINNSQAVGNS----- 189
Db 325 PAARSETLGFYPMKPIIPTPMWRYFQWDRLLPSH-----TGTSGTPTNYHGTDPDD 378
QY 190 -SFYCLB-YPPSQMLRTGNPF--TF-----SYFEE-----VFPSSVAHSQSL 229
Db 379 VQFTTENSVPVHLRTGDEFATGTFFDCKPCRLTHTWQTNRLGLPPLNLSLPQSBGA 438
QY 230 DR-----LMNPILIDYL--YYLNRTONS----- 251
Db 439 TNFGDIGVQDKRGVYQWNTDVTYATITMRPAVGVSAFYSPFASSTQGFPTIAAG 498
QY 252 -GSAQNKLFLRSRSPAGMSVQPKWLPQCY--RQORVSKTIDNNNSFTWTGASKY 307
Db 499 RGAQTDEMQAADDPR-----YAGRGHQKQTTTGTGETPERFTY----- 538
QY 308 NLNGRESINGTAMASHKDEDKFPPMSGVMIFGXSAGASNTALD-NVMITDEBEIKA 366
Db 539 -----IAHQDT-----GRIPAGWIONINPNLPTVDNVLLP 570
QY 367 TNVPATERFGTVAVNFOSSSTDPAATGDVHAMGALPGMWODRDVYLOGPIWAKIPTHG 426
Db 571 TDPIG-----GKTGINY--TNFNHYGLTALNNVP-----PYRPGQIWDKFPDID- 615
QY 427 FHSPLMGFGFLK-----NPPQILIKNTPVPA--PPAESATFPASFIT 470
Db 616 -----LKRLLHNAFVVCNNCPQLFFKVAPNLTNEBDPASANMSR-----IV 660
QY 471 QYSTGVSEIEMELOKENSRRNPEVOYTSNYAKSANDPTVNNGLYTPRPIG 526
Db 661 TYSDFWKKGLVFRKAKLRASHTNPIQOMSIN-----VDNQFNLYL-PNNIG 705

RESULT 13

VCPV1F

coat protein VP1 - feline panleukopenia virus

N:Contains: coat protein VP2

C:Species: feline panleukopenia virus, FPLV

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #ext_change 09-Jul-2004

C:Accession: A03701

R:Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.

J. Virol. 55, 574-587, 1985

A:Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv

A:Reference number: A03697; MUID:85265017; PMID:2991581

A:Accession: A03701

A:Molecule type: DNA

A:Residues: 1-727 <CAR>

A:Cross-references: UNIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:G333474; PID

C:Genetics:

A:Introns: 11/1

C:Superfamily: parvovirus coat protein

C:Keyword: coat protein

F:144-727/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.7%; Score 194; DB 1; Length 727;

Best Local Similarity 20.7%; Pred. No. 3.1e-06;

Matches 136; Conservative 73; Mismatches 215; Indels 232; Gaps 32;

5 GGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTTST-----RTWALPTNN- 52

153 GGCP -AVNBERATGSGNGSGGGGGG--GGVIGISTGTNNOTEFKFLNGVETIANS 209

53 ---HL-----YKQI-----SSASTGASNDNHFGYSTPWCYDFNRFCHSPRW 95

210 RLVLHLMPESENYRVRVNNMDKTAVKGNMALLDTHQIVTPWSLVDANAMGVWFNPGW 269

96 QRLNNNGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNTSTVOYFSDSEYOLPYV 152

270 QLVNVTMSBLHVSFEQEIFNVVLKTVSESAIOPPTKYNNNDLTASLWALDSNNMTPT 329

153 LGSANQGL-----PPFPA-----DVFMIPQYGLTLNNGSAVGRS----- 189

330 PAMRSETLGFYPMKPTLPTPRRYFFQMDRLILPSH-----TGTSGTPTNIYHGTDPD 383

190 -SFYCLE-YFPQMLRTGNF---TF-----SYTEE-----VPHSSYAHQSOL 229

384 VQFYTIENSVPRLHRTGDEFATGTFPDCPKRLHTHTWQTNRALGLPPLNSLPOSEGA 443

230 DR-----LMNPLIOYL---YYLNRTQNS----- 251

444 TNFGDIGVQDKRRGVTOMGNTDYTEATTMRPAEVGSAFYSPFASSTGCPKTIPLAG 503

252 -GSAONKDLILFSRSGPAGMSVOPKMLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY 307

504 RGAQIDENQAAGDR-----YAFGQHOGKTTTGTTPRFFY----- 543

308 NLNGRESIINPTGAMASHKODEKFFPMGSMVIFGESAGASNTALD-NVMTIDEEIKA 366

544 -----LAHQDT-----GRYPAGDWIQININFLPVTNDVLLP 575

367 TNVATERPGTVAVNPOSSSTDPAEDVHAMGALPGWVQDRDYLQGPWAKIPIHTDGH 426

576 TDEIG-----GKTGINY--TNIFMTYGPILALNVP-----PVYPNGQIWDKEPDTD- 620

427 FHSPILMGFGFLK-----NPPQILIKNTVPAN---PPAEFSATKFAFIT 470

621 -----LKRHLHVAAPFVQCNCPQGLFVKVAPNLINTEYDPPASANMR-----IV 665

471 QYSTGVSEIEMELQENSKRNPEVOYTSNAXKANVDTYDNNGLYTEPRPIG 526

666 TYSDFMWKGLTVFKAIRASHTWNPLOQMSIN-----VDNQFNVL-PNNIG 710

Db

Qy

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C:Species: canine parvovirus, CPV

C:Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S49594

R:Mizak, B.; Plucienniczak, A.

submitted to the EMBL Data Library, November 1994

A:Description: Polish isolates of canine parvovirus.

A:Reference number: S49594

A:Accession: S49594

A:Molecule type: DNA

A:Residues: 1-584 <MIZ>

A:Cross-references: UNIPROT:Q66208; UNIPARC:UPI00000FA046; EMBL:246651; NID:G572660; PID

C:Superfamily: parvovirus coat protein

Query Match 6.5%; Score 189; DB 2; Length 584;

Best Local Similarity 20.8%; Pred. No. 5.2e-06;

Matches 132; Conservative 89; Mismatches 223; Indels 192; Gaps 33;

5 GGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTTST-----RTWALPTNN- 52

10 GGCP -AVNBERATGSGNGSGGGGGG--GGVIGISTGTNNOTEFKFLNGVETIANS 66

53 ---HL-----YKQI-----SSASTGASNDNHFGYSTPWCYDFNRFCHSPRW 95

67 RLVLHLMPESENYRVRVNNMDKTAVKGNMALLDTHQIVTPWSLVDANAMGVWFNPGW 126

96 QRLNNNGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNTSTVOYFSDSEYOLPYV 152

127 QLVNVTMSBLHVSFEQEIFNVVLKTVSESAIOPPTKYNNNDLTASLWALDSNNMTPT 186

153 LGSANQGL-----PPFPA-----DVFMIPQYGLTLNNGSAVGRS----- 189

187 PAMRSETLGFYPMKPTLPTPRRYFFQMDRLILPSH-----TGTSGTPTNIYHGTDPD 240

190 -SFYCLE-YFPQMLRTGNF-TFSYTEBEVPHSSYAHQSOLDLNMLDIOYLYLNR 246

241 VQFYTIENSVPRLHRTGDEFATGTFPDCPK--CRLHTWQTNRALG--LPPFLNSLPO 296

247 TONQS-----GSAONK-----DLFBSRSGAGMSVOPKMLPGPCYRQGV 287

297 SEGCTNFGYIGVQDKRRGVTOMGNTNYTEATTMRPAEVGS-----APYSFEAS 348

288 SK-----TKTDNNNSNFTWTGASKY---NLNGRESIINPT---AMASHKD 327

349 TGCPKFTPIAAGRGAGQIDENQA---DQDPYIACRGHQGTITTTGTTPRFFYIAHD 405

406 T-----GRYPGDMWIQININFLPVTNDVLLPTDPIG---GKTGINY--TN 446

387 TDPATGDVHAMGALPGWVQDRDYLQGPWAKIPIHTDGHFHPSPILMGFGFLK----- 439

447 IENTYGPILALNVP-----PVYPNGQIWDKEPDTD-----LKRHLHVA 486

440 -----NPPQILIKNTVPAN---PPAEFSATKFAFITOYSTGVSEIEMELQENS 490

487 PFCVQNNCPGOLFVKVAPNLINTEYDPPASANMR-----LVYISDFMWKGLTVFKAIRAS 542

491 KRNPEVOYTSNAXKANVDTYDNNGLYTEPRPIG 526

543 HTWNPLOQMSIN-----VDNQFNVL-PSNIG 567

Db

Qy

Db

Qy

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RESULT 15

VCPV1F

coat protein VP1 - feline panleukopenia virus (strain 193)

N:Contains: coat protein VP2

C:Species: feline panleukopenia virus, FPLV

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 09-Jul-2004

C:Accession: B36608

R:Marlyn, J.C.; Davidson, B.B.; Studdert, M.J.

J. Gen. Virol. 71, 2747-2753, 1990

A:Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parv.

A:Reference number: A36608; MUID:91073139; PMID:2174965

C:Superfamily: parvovirus coat protein

Query Match 6.5%; Score 189; DB 2; Length 584;

Best Local Similarity 20.8%; Pred. No. 5.2e-06;

Matches 132; Conservative 89; Mismatches 223; Indels 192; Gaps 33;

5 GGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTTST-----RTWALPTNN- 52

10 GGCP -AVNBERATGSGNGSGGGGGG--GGVIGISTGTNNOTEFKFLNGVETIANS 66

53 ---HL-----YKQI-----SSASTGASNDNHFGYSTPWCYDFNRFCHSPRW 95

67 RLVLHLMPESENYRVRVNNMDKTAVKGNMALLDTHQIVTPWSLVDANAMGVWFNPGW 126

96 QRLNNNGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNTSTVOYFSDSEYOLPYV 152

127 QLVNVTMSBLHVSFEQEIFNVVLKTVSESAIOPPTKYNNNDLTASLWALDSNNMTPT 186

153 LGSANQGL-----PPFPA-----DVFMIPQYGLTLNNGSAVGRS----- 189

187 PAMRSETLGFYPMKPTLPTPRRYFFQMDRLILPSH-----TGTSGTPTNIYHGTDPD 240

190 -SFYCLE-YFPQMLRTGNF-TFSYTEBEVPHSSYAHQSOLDLNMLDIOYLYLNR 246

241 VQFYTIENSVPRLHRTGDEFATGTFPDCPK--CRLHTWQTNRALG--LPPFLNSLPO 296

247 TONQS-----GSAONK-----DLFBSRSGAGMSVOPKMLPGPCYRQGV 287

297 SEGCTNFGYIGVQDKRRGVTOMGNTNYTEATTMRPAEVGS-----APYSFEAS 348

288 SK-----TKTDNNNSNFTWTGASKY---NLNGRESIINPT---AMASHKD 327

349 TGCPKFTPIAAGRGAGQIDENQA---DQDPYIACRGHQGTITTTGTTPRFFYIAHD 405

406 T-----GRYPGDMWIQININFLPVTNDVLLPTDPIG---GKTGINY--TN 446

387 TDPATGDVHAMGALPGWVQDRDYLQGPWAKIPIHTDGHFHPSPILMGFGFLK----- 439

447 IENTYGPILALNVP-----PVYPNGQIWDKEPDTD-----LKRHLHVA 486

440 -----NPPQILIKNTVPAN---PPAEFSATKFAFITOYSTGVSEIEMELQENS 490

487 PFCVQNNCPGOLFVKVAPNLINTEYDPPASANMR-----LVYISDFMWKGLTVFKAIRAS 542

491 KRNPEVOYTSNAXKANVDTYDNNGLYTEPRPIG 526

543 HTWNPLOQMSIN-----VDNQFNVL-PSNIG 567

Db

Qy

Db

Qy

Db

Qy

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Qy

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A:Accession: B36608
A:Molecule type: DNA
A:Residues: 1-727 <MAR>
A:Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:144-727/Product: coat protein VP2 #status predicted <VP2>

Query Match 6.5%; Score 189; DB 1; Length 727;
Best Local Similarity 20.6%; Pred. No. 7,2e-06;
Matches 135; Conservative 73; Mismatches 216; Indels 232; Gaps 32;

```
QY 5 GGAPNADNNEGADVGNASGNMHCSTWLGDRVITTTST-----RTMALPTVNN- 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 GGQP-AVNERATGSGNSGGGGGGS--GGVIGISTGFNNQTEPKFLENGVEITANSS 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 53 ---HL-----YKQI-----SSASTGASNDNHFGYSTPWFYFDNRFHCHSPRDW 95
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 210 RLVLHMPESSENYKRVVNNMDKTAVKGMALDIDHVOIVTFPWSLVDANAMGVWFNPQDW 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 96 QRLINNNNGFRPKRLNFKLNFQVKEVT---TNDGVTTIANLITSTVQVFSDEYQLPYV 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 270 QILVNTMSLHLVSEFQELFNVVLKTVSESATQPTKYVNDLTASLMLVALDSNNTMPPT 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 153 LGSATQGCY-----PPFPA-----DVFMIPQGYLLNNGSQAVGRS----- 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 330 PAAMSSEITGFPMKPTIPTPMRYVFPQMDRTLIIPSH-----TGTSGTPTVYHGTDPDD 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 -SFYCLE-YFSPQMLRTGNF--TF-----SYTFEE-----VPEHSSVYHSQSL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 VQFYTIENSVPVHLRLRTGDEFATGTFEPDCKPCRLHTWQTRALGLPPFLNLSLPQSEGA 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 DR-----LMNPLIDQYL--YLNRTQNS----- 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 444 TNFGDIGVQODKRGVTOQMGNTDYITBATIMRPAEYISAPYSEASTQGFPTPIAAG 503
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 252 -GSAQNKDLLFSRGSPPAGMSVQPKWLPQPCY---RQQRVSKTKTDNNNSNFTWTGASKY 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 504 RGAQTDENQADGDR-----YAFGRQHQKTTTGTGTPERTTY----- 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 NINGRESIINPGTAMASHKDEDEKFFPMSCVMI FGESAGASNTALD-NVMITDEEETKA 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 -----IAHQDT-----GRYPEGDWIQININFLPVTNDNVLLP 575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 TNPVATERGRTVAVNFQSSSTDPATGDVHAMGALPGMTWQDRDYYLQGIWAKIPIHTDGH 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 TDPFG--GKTGINY--TNIFNTYGPLTALNNVP-----PVYPNGQIMDKPEPTD-- 620
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 FHPSPLMGSGFLK-----NPPQILIKNTVPVPAN---PPAEFSATKPFASFT 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 621 -----LKPRLHVVAFFVQCNCPQQLFVKVAPRLTNEYDPDASANMSR-----IV 665
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 471 QYSTQVSVIEIEMELQKENSKRMPREVOYTSNYAKSANDFTVDNNGLYTEBPRPTG 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 666 TYSDFMWKGLVFKAKLIRASHMTNPICQWSIN-----VDNQFNVV--PNNIG 710
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: November 23, 2005, 17:44:04
Job time : 20.8571 secs

Db 563 EEEIKATNPVATERGTYAVVNFQSSSTDPATCDVAMALPGMWQDDVYLQGIWAKI 622
Qy 421 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 480
Db 623 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 682
Qy 481 IEMELQKENSKRMPNEVOYTSNYAKSANVDFTVDNNGLYTEBRPIGTRYLTRPL 534
Db 683 IEMELQKENSKRMPNEVOYTSNYAKSANVDFTVDNNGLYTEBRPIGTRYLTRPL 736

RESULT 2

06JC12_VIRU PRELIMINARY; PRT; 736 AA.
AC 06JC12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvirra M.R., Lu Y., Calcedo R., Zhou X., Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human tissues";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530607; AAS99292.1; -; Genomic_DNA.
DR SMR; Q6JC12; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81364 MW; F2D75A06662B6376 CRC64;

Query Match 99.5%; Score 2892; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 1.3e-202;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MASGGGAPMADNBNBAGDVGNAAGNMHCDSTWLGDRVITTSRTTALPTNNHLYKQISS 60
Db 203 MASGGGAPMADNBNBAGDVGNAAGNMHCDSTWLGDRVITTSRTTALPTNNHLYKQISS 262
Qy 61 ASTGASNDNHFGYSTPMGYDFPNRPHCHFSPRDMQRLINNMGFRPKLNFKLNIQVK 120
Db 263 ASTGASNDNHFGYSTPMGYDFPNRPHCHFSPRDMQRLINNMGFRPKLNFKLNIQVK 322
Qy 121 EYTTNDGVTIANNLITSTVOVFSDBEYQLPYVLGSAHQGCLPPPADVFMIPOGYLTIN 180
Db 323 EYTTNDGVTIANNLITSTVOVFSDBEYQLPYVLGSAHQGCLPPPADVFMIPOGYLTIN 382
Qy 181 NSGQAVGRSSFYCLEYFPSSQMLRTGNFTFSYTFEEVPHSSYAHSSQSLDRLMNPIDQY 240
Db 383 NSGQAVGRSSFYCLEYFPSSQMLRTGNFTFSYTFEEVPHSSYAHSSQSLDRLMNPIDQY 442
Qy 241 LYYLNRTONOGSAGAKNKLFLSRGSPAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSNT 300
Db 443 LYYLNRTONOGSAGAKNKLFLSRGSPAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSNT 502
Qy 301 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMSGVMIFGKESAGASNTALDNVMTD 360
Db 503 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMSGVMIFGKESAGASNTALDNVMTD 562
Qy 361 EEEIKATNPVATERGTYAVVNFQSSSTDPATCDVAMALPGMWQDDVYLQGIWAKI 420
Db 563 EEEIKATNPVATERGTYAVVNFQSSSTDPATCDVAMALPGMWQDDVYLQGIWAKI 622
Qy 421 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 480

Db 623 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 682
Qy 481 IEMELQKENSKRMPNEVOYTSNYAKSANVDFTVDNNGLYTEBRPIGTRYLTRPL 534
Db 683 IEMELQKENSKRMPNEVOYTSNYAKSANVDFTVDNNGLYTEBRPIGTRYLTRPL 736

RESULT 3

06JC08_VIRU PRELIMINARY; PRT; 736 AA.
AC 06JC08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvirra M.R., Lu Y., Calcedo R., Zhou X., Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human tissues";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530611; AAS99296.1; -; Genomic_DNA.
DR SMR; Q6JC08; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD CRC64;

Query Match 99.3%; Score 2885; DB 2; Length 736;
Best Local Similarity 99.1%; Pred. No. 4.3e-202;
Matches 529; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MASGGGAPMADNBNBAGDVGNAAGNMHCDSTWLGDRVITTSRTTALPTNNHLYKQISS 60
Db 203 MASGGGAPMADNBNBAGDVGNAAGNMHCDSTWLGDRVITTSRTTALPTNNHLYKQISS 262
Qy 61 ASTGASNDNHFGYSTPMGYDFPNRPHCHFSPRDMQRLINNMGFRPKLNFKLNIQVK 120
Db 263 TSTGASNDNHFGYSTPMGYDFPNRPHCHFSPRDMQRLINNMGFRPKLNFKLNIQVK 322
Qy 121 EYTTNDGVTIANNLITSTVOVFSDBEYQLPYVLGSAHQGCLPPPADVFMIPOGYLTIN 180
Db 323 EYTTNDGVTIANNLITSTVOVFSDBEYQLPYVLGSAHQGCLPPPADVFMIPOGYLTIN 382
Qy 181 NSGQAVGRSSFYCLEYFPSSQMLRTGNFTFSYTFEEVPHSSYAHSSQSLDRLMNPIDQY 240
Db 383 NSGQAVGRSSFYCLEYFPSSQMLRTGNFTFSYTFEEVPHSSYAHSSQSLDRLMNPIDQY 442
Qy 241 LYYLNRTONOGSAGAKNKLFLSRGSPAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSNT 300
Db 443 LYYLNRTONOGSAGAKNKLFLSRGSPAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSNT 502
Qy 301 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMSGVMIFGKESAGASNTALDNVMTD 360
Db 503 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMSGVMIFGKESAGASNTALDNVMTD 562
Qy 361 EEEIKATNPVATERGTYAVVNFQSSSTDPATCDVAMALPGMWQDDVYLQGIWAKI 420
Db 563 EEEIKATNPVATERGTYAVVNFQSSSTDPATCDVAMALPGMWQDDVYLQGIWAKI 622
Qy 421 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 480
Db 623 PHTDGHFHPSPLMGFGGLKNPPOLLIKNTVPANPAPAEFSATKASFTIQTSTQVSE 682
Qy 481 IEMELQKENSKRMPNEVOYTSNYAKSANVDFTVDNNGLYTEBRPIGTRYLTRPL 534

Db 683 IEMELQKENSKRNNPEVOYTSNYAKSANYDFTVDNNGLYTEPRPIGTRYLTRPL 736

RESULT 4
ID 056137_9VIRU PRELIMINARY; PRT; 736 AA.

AC 056137;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein VPI.
OS Adeno-associated virus 6.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
NCBI_TaxID=68558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98080418; PubMed=9420229;
RA Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2.";
RL J. Virol. 72:309-319(1998).
DR EMBL; AF028704; AAB95550.1; -; Genomic_DNA.
DR SMR; 056137; 217-736.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo coat.
DR Pfam; PF00740; Parvo coat; 1.
SQ SEQUENCE 736 AA; 81411 MW; 311217A089C565F5 CRC64;

Query Match 99.2%; Score 2884; DB 2; Length 736;
Best Local Similarity 99.1%; Pred. No. 5e-202;
Matches 529; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASGGAPMADNNEGADGVNASGNWCHDSTWLGDRVITTSRTTALPTNNHLYQIIS 60
DB 203 MASGGAPMADNNEGADGVNASGNWCHDSTWLGDRVITTSRTTALPTNNHLYQIIS 262
QY 61 ASTGASNDNHYFGYSTPMGYPFDRNRFCHFSPPDMQRLINNMGFPKRLNFKLFNIQVK 120
DB 263 ASTGASNDNHYFGYSTPMGYPFDRNRFCHFSPPDMQRLINNMGFPKRLNFKLFNIQVK 322
QY 121 EVTTNDGVTTIANNLSTVQVPSDSEYQLPYVIGSAHQGLPPPADVPMIPOYGYLTIN 180
DB 323 EVTTNDGVTTIANNLSTVQVPSDSEYQLPYVIGSAHQGLPPPADVPMIPOYGYLTIN 382
QY 181 NSQAVGRSSFYCLEFPPSQMLRTGNNFTFSYFEEVPHSSVAHSQSILRLNPLIDQY 240
DB 383 NSQAVGRSSFYCLEFPPSQMLRTGNNFTFSYFEEVPHSSVAHSQSILRLNPLIDQY 442
QY 241 LYYLNTONOSGSAQNKKDLFSRGSFAGMSVQPKMLPGCYRQORVSKTKTDNNNSNFT 300
DB 443 LYYLNTONOSGSAQNKKDLFSRGSFAGMSVQPKMLPGCYRQORVSKTKTDNNNSNFT 502
QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDNVMTD 360
DB 503 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDNVMTD 562
QY 361 EBEIKATNPVATERFGTVAANFOSSSTDPAITGVHAMGALPGMWQDRDYLLQPIYAKI 420
DB 563 EBEIKATNPVATERFGTVAANFOSSSTDPAITGVHAMGALPGMWQDRDYLLQPIYAKI 622
QY 421 PHTDGHFHPBLMGFGELKNPPQILIKNTPVANPAPAESATKFAFITQYSTGQSV 480
DB 623 PHTDGHFHPBLMGFGELKNPPQILIKNTPVANPAPAESATKFAFITQYSTGQSV 682
QY 481 IEMELQKENSKRNNPEVOYTSNYAKSANYDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB 683 IEMELQKENSKRNNPEVOYTSNYAKSANYDFTVDNNGLYTEPRPIGTRYLTRPL 736

RESULT 5
06JC13_9VIRU

ID 06JC13_9VIRU PRELIMINARY; PRT; 737 AA.

AC 06JC13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VPI.
CN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530606; AAS99291.1; -; Genomic_DNA.
DR SMR; 06JC13; 218-737.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo coat.
DR Pfam; PF00740; Parvo coat; 1.
SQ SEQUENCE 737 AA; 81332 MW; 94CED0F3AFD6E492 CRC64;

Query Match 99.2%; Score 2883; DB 2; Length 737;
Best Local Similarity 99.3%; Pred. No. 6e-202;
Matches 530; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASGGAPMADNNEGADGVNASGNWCHDSTWLGDRVITTSRTTALPTNNHLYQIIS 60
DB 204 MASGGAPMADNNEGADGVNASGNWCHDSTWLGDRVITTSRTTALPTNNHLYQIIS 263
QY 61 ASTGASNDNHYFGYSTPMGYPFDRNRFCHFSPPDMQRLINNMGFPKRLNFKLFNIQVK 120
DB 264 ASTGASNDNHYFGYSTPMGYPFDRNRFCHFSPPDMQRLINNMGFPKRLNFKLFNIQVK 323
QY 121 EVTTNDGVTTIANNLSTVQVPSDSEYQLPYVIGSAHQGLPPPADVPMIPOYGYLTIN 180
DB 324 EVTTNDGVTTIANNLSTVQVPSDSEYQLPYVIGSAHQGLPPPADVPMIPOYGYLTIN 383
QY 181 NSQAVGRSSFYCLEFPPSQMLRTGNNFTFSYFEEVPHSSVAHSQSILRLNPLIDQY 240
DB 384 NSQAVGRSSFYCLEFPPSQMLRTGNNFTFSYFEEVPHSSVAHSQSILRLNPLIDQY 443
QY 241 LYYLNTONOSGSAQNKKDLFSRGSFAGMSVQPKMLPGCYRQORVSKTKTDNNNSNFT 300
DB 444 LYYLNTONOSGSAQNKKDLFSRGSFAGMSVQPKMLPGCYRQORVSKTKTDNNNSNFT 503
QY 301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDNVMTD 360
DB 504 WTGASKYNLNGRESIINPGTAMASHKDEDEKFFPMGCVMI FGKESAGASTALDNVMTD 563
QY 361 EBEIKATNPVATERFGTVAANFOSSSTDPAITGVHAMGALPGMWQDRDYLLQPIYAKI 420
DB 564 EBEIKATNPVATERFGTVAANFOSSSTDPAITGVHAMGALPGMWQDRDYLLQPIYAKI 623
QY 421 PHTDGHFHPBLMGFGELKNPPQILIKNTPVANPAPAESATKFAFITQYSTGQSV 480
DB 624 PHTDGHFHPBLMGFGELKNPPQILIKNTPVANPAPAESATKFAFITQYSTGQSV 683
QY 481 IEMELQKENSKRNNPEVOYTSNYAKSANYDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB 684 IEMELQKENSKRNNPEVOYTSNYAKSANYDFTVDNNGLYTEPRPIGTRYLTRPL 737

RESULT 6
06JC10_9VIRU
ID 06JC10_9VIRU PRELIMINARY; PRT; 736 AA.
AC 06JC10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
Wilson J.M.,
RT "Clades of Adeno-associated viruses are widely disseminated in human
tissues".
RL J. Virol. 78:6381-6388(2004).
DR EMBL: AY530609; AAS9294.1; -; Genomic_DNA.
DR SMR: Q6UC10; 217-736.
DR GO: GO:0019028; C:viral capsid; IEA.
DR InterPro: IPR001403; Parvovir. coat.
DR Pfam: PF00740; Parvovir. coat; 1.
SQ SEQUENCE 736 AA; 81388 MW; BA9463E970028DF0 CRC64;

Query Match 98.5%; Score 2863; DB 2; Length 736;
Best Local Similarity 98.9%; Pred. No. 1.7e-200;
Matches 528; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MASGGAPMADNNGAGDVGNGASGNMHCDSMTLGDRTVITSTRMALPTYNHLYKQISS 60
DB 203 MASGGAPMADNNGAGDVGNGASGNMHCDSMTLGDRTVITSTRMALPTYNHLYKQISS 262
QY 61 ASTGASNDNHFGYSTPMGYFDNFRFCHFSRPRDQRLINNNMGRPRKLNFKLFNIQVK 120
DB 263 ASTGASNDNHFGYSTPMGYFDNFRFCHFSRPRDQRLINNNMGRPRKLNFKLFNIQVK 322
QY 121 ETTNDGVTIANNLITSTVQVFSDEYQLPYVLGSAHQGLPPPADYFMIPQYGYLTIN 180
DB 323 ETTNDGVTIANNLITSTVQVFSDEYQLPYVLGSAHQGLPPPADYFMIPQYGYLTIN 382
QY 181 NGSQAVGRSSFYCYLFFPSQMLRTGNNTFESTFEVPHSSYAHSSQSLDRMLNPDIQY 240
DB 383 NGSQAVGRSSFYCYLFFPSQMLRTGNNTFESTFEVPHSSYAHSSQSLDRMLNPDIQY 442
QY 241 LYYLNRTONOGSGAQNKKLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSFT 300
DB 443 LYYLNRTONOGSGAQNKKLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSFT 502
QY 301 WTGASKYINLNGRESIINPGTAMASHKDEDEKFFPMGVTMFGKESAGASNTALDNVMTD 360
DB 503 WTGASKYINLNGRESIINPGTAMASHKDEDEKFFPMGVTMFGKESAGASNTALDNVMTD 562
QY 361 EEBIRATNPVATERPGTAVAVNFOSSTDPATGDVHAMGALPGMWQODRDVYLOGPIMAKI 420
DB 563 EEBIRATNPVATERPGTAVAVNFOSSTDPATGDVHAMGALPGMWQODRDVYLOGPIMAKI 622
QY 421 PHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTGQSVVE 480
DB 623 PHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTGQSVVE 682
QY 481 IEMELQKENSKRWNPEVQYTSNYAKSANDFTVDNNGLYTEBRPIGTRYLRLPL 534
DB 683 IEMELQKENSKRWNPEVQYTSNYAKSANDFTVDNNGLYTEBRPIGTRYLRLPL 736
RESULT 7
Q6UC34_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6UC34;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Capsid protein VP1.
OS Adeno-associated virus.
GN Name=cap;
OX NCBI_TaxId=272636;
RP NUCLEOTIDE SEQUENCE.

OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
Wilson J.M.,
RT "Clades of Adeno-associated viruses are widely disseminated in human
tissues".
RL J. Virol. 78:6381-6388(2004).
DR EMBL: AY530585; AAS9270.1; -; Genomic_DNA.
DR SMR: Q6UC34; 217-735.
DR GO: GO:0019028; C:viral capsid; IEA.
DR InterPro: IPR001403; Parvovir. coat.
DR Pfam: PF00740; Parvovir. coat; 1.
SQ SEQUENCE 735 AA; 81962 MW; 85DC69C5523D983 CRC64;

Query Match 87.3%; Score 2536.5; DB 2; Length 735;
Best Local Similarity 85.2%; Pred. No. 1.3e-176;
Matches 455; Conservative 34; Mismatches 44; Indels 1; Gaps 1;

QY 1 MASGGAPMADNNGAGDVGNGASGNMHCDSMTLGDRTVITSTRMALPTYNHLYKQISS 60
DB 203 MASGGAPMADNNGAGDVGNGASGNMHCDSMTLGDRTVITSTRMALPTYNHLYKQISS 262
QY 61 ASTGASNDNHFGYSTPMGYFDNFRFCHFSRPRDQRLINNNMGRPRKLNFKLFNIQVK 120
DB 263 OS-QASNDNHFGYSTPMGYFDNFRFCHFSRPRDQRLINNNMGRPRKLNFKLFNIQVK 321
QY 121 ETTNDGVTIANNLITSTVQVFSDEYQLPYVLGSAHQGLPPPADYFMIPQYGYLTIN 180
DB 322 ETTNDGVTIANNLITSTVQVFSDEYQLPYVLGSAHQGLPPPADYFMIPQYGYLTIN 381
QY 181 NGSQAVGRSSFYCYLFFPSQMLRTGNNTFESTFEVPHSSYAHSSQSLDRMLNPDIQY 240
DB 382 NGSQAVGRSSFYCYLFFPSQMLRTGNNTFESTFEVPHSSYAHSSQSLDRMLNPDIQY 441
QY 241 LYYLNRTONOGSGAQNKKLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSFT 300
DB 442 LYYLNRTONOGSGAQNKKLLFSRGSFAGMSVOPKMWLPGPCYRQORVSKTKTDNNNSFT 501
QY 301 WTGASKYINLNGRESIINPGTAMASHKDEDEKFFPMGVTMFGKESAGASNTALDNVMTD 360
DB 502 WTGASKYINLNGRESIINPGTAMASHKDEDEKFFPMGVTMFGKESAGASNTALDNVMTD 561
QY 361 EEBIRATNPVATERPGTAVAVNFOSSTDPATGDVHAMGALPGMWQODRDVYLOGPIMAKI 420
DB 562 EEBIRATNPVATERPGTAVAVNFOSSTDPATGDVHAMGALPGMWQODRDVYLOGPIMAKI 621
QY 421 PHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTGQSVVE 480
DB 622 PHTDGHFHPSPLMGFGGLKNPPOILLIKNTVPANPAPAFSATKFSFITYSTGQSVVE 681
QY 481 IEMELQKENSKRWNPEVQYTSNYAKSANDFTVDNNGLYTEBRPIGTRYLRLPL 534
DB 682 IEMELQKENSKRWNPEVQYTSNYAKSANDFTVDNNGLYTEBRPIGTRYLRLPL 735
RESULT 8
Q67008_9VIRU PRELIMINARY; PRT; 735 AA.
AC Q67008;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxId=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Chen C.L., Jensen R.L., Schnepp B.C., Connell M.J., Bartlett J.S.,
RA Sfeera T.J., Shell R., Johnson P.R., Clark K.R.,
RT "Characterization of Adeno-Associated Viruses in Children."
RL Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY695376; AU05370.1; -; Genomic_DNA.
DR SMR: Q67008; 217-735.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo coat.
DR Pfam: PF00740; Parvo coat; 1.
SQ SEQUENCE 735 AA; 81887 MW; 258BFB955F1C9925 CRC64;

Query Match 87.3%; Score 2535.5; DB 2; Length 735;
Best Local Similarity 85.2%; Pred. No. 1.5e-176;
Matches 455; Conservative 34; Mismatches 44; Indels 1; Gaps 1;

QY 1 MASGGAPMADNNEGADGVGNASGNMHCSTWLGDRVITSTRTWMLPTYNHLYQOIS 60
DB 203 MASGGAPMADNNEGADGVGNSSGNMHCDSQWLGDRVITSTRTWMLPTYNHLYQOIS 262
QY 61 ASTGASNDNHFGYSTPMGTFDNRPHCHFSPRDMQRLINNMWGFPRKLNFLFNIOVK 120
DB 263 QS-GASNDNHFGYSTPMGTFDNRPHCHFSPRDMQRLINNMWGFPRKLNFLFNIOVK 321
QY 121 EYVNDGVTITANNLTSTVQVPSDSYQLPYVLGSAHQCLPPPADVFMIPQYGYLTN 180
DB 322 EYVNDGVTITANNLTSTVQVFTDSEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTN 381
QY 181 NSQVAGRSFYCLFEPFSGMRLTGNNFTFSEVPHSSVYHSSQSLDRLNPLIDQY 240
DB 382 NSQVAGRSFYCLFEPFSGMRLTGNNFTFSEVPHSSVYHSSQSLDRLNPLIDQY 441
QY 241 LYLNTQNSGSAQNKDLFFSRGSPAGMSVQPKMLPGPCYRQORVSKTKTDNNNSNFT 300
DB 442 LYLNTQNSGSAQNKDLFFSRGSPAGMSVQPKMLPGPCYRQORVSKTKTDNNNSNFT 501
QY 301 WTGASKTYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDNYMTD 360
DB 502 WTGASKTYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDNYMTD 561
QY 361 EBEIKATNPVATERFCTVAVNPOSSSTDPAITGVNHMGALPGWMDRDVYLOGPIWAKI 420
DB 562 EBEIKATNPVATERFCTVAVNPOSSSTDPAITGVNHMGALPGWMDRDVYLOGPIWAKI 621
QY 421 PHTDGHFHPSPPLMGGFGLKMPPOQLIKNTVPANPAEFSATKFSFITQYSTGVSV 480
DB 622 PHTDGHFHPSPPLMGGFGLKMPPOQLIKNTVPANPAEFSATKFSFITQYSTGVSV 681
QY 481 IEMELQENSKRNPNPEVQYTSNYSKASANDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB 682 IEMELQENSKRNPNPEVQYTSNYSKASANDFTVDNNGLYTEPRPIGTRYLTRPL 735
RESULT 9
Q6JC28 9VIRU
ID Q6JC28 9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JC28
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VPI.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues." J. Virol. 78:6381-6388 (2004).

DR EMBL: AY510591; AA599276.1; -; Genomic_DNA.
DR SMR: Q6JC28; 217-735.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo coat.
DR Pfam: PF00740; Parvo coat; 1.
SQ SEQUENCE 735 AA; 81897 MW; 197066F8911FAE9B CRC64;

Query Match 87.1%; Score 2532.5; DB 2; Length 735;
Best Local Similarity 85.0%; Pred. No. 2.5e-176;
Matches 454; Conservative 34; Mismatches 45; Indels 1; Gaps 1;

QY 1 MASGGAPMADNNEGADGVGNASGNMHCSTWLGDRVITSTRTWMLPTYNHLYQOIS 60
DB 203 MASGGAPMADNNEGADGVGNSSGNMHCDSQWLGDRVITSTRTWMLPTYNHLYQOIS 262
QY 61 ASTGASNDNHFGYSTPMGTFDNRPHCHFSPRDMQRLINNMWGFPRKLNFLFNIOVK 120
DB 263 QS-GASNDNHFGYSTPMGTFDNRPHCHFSPRDMQRLINNMWGFPRKLNFLFNIOVK 321
QY 121 EYVNDGVTITANNLTSTVQVPSDSYQLPYVLGSAHQCLPPPADVFMIPQYGYLTN 180
DB 322 EYVNDGVTITANNLTSTVQVFTDSEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTN 381
QY 181 NSQVAGRSFYCLFEPFSGMRLTGNNFTFSEVPHSSVYHSSQSLDRLNPLIDQY 240
DB 382 NSQVAGRSFYCLFEPFSGMRLTGNNFTFSEVPHSSVYHSSQSLDRLNPLIDQY 441
QY 241 LYLNTQNSGSAQNKDLFFSRGSPAGMSVQPKMLPGPCYRQORVSKTKTDNNNSNFT 300
DB 442 LYLNTQNSGSAQNKDLFFSRGSPAGMSVQPKMLPGPCYRQORVSKTKTDNNNSNFT 501
QY 301 WTGASKTYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDNYMTD 360
DB 502 WTGASKTYNLNGRESIINPGTAMASHKODEDKFFPMGCVMI FGKESAGASNTALDNYMTD 561
QY 361 EBEIKATNPVATERFCTVAVNPOSSSTDPAITGVNHMGALPGWMDRDVYLOGPIWAKI 420
DB 562 EBEIKATNPVATERFCTVAVNPOSSSTDPAITGVNHMGALPGWMDRDVYLOGPIWAKI 621
QY 421 PHTDGHFHPSPPLMGGFGLKMPPOQLIKNTVPANPAEFSATKFSFITQYSTGVSV 480
DB 622 PHTDGHFHPSPPLMGGFGLKMPPOQLIKNTVPANPAEFSATKFSFITQYSTGVSV 681
QY 481 IEMELQENSKRNPNPEVQYTSNYSKASANDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB 682 IEMELQENSKRNPNPEVQYTSNYSKASANDFTVDNNGLYTEPRPIGTRYLTRPL 735
RESULT 10
Q6JB27 9VIRU
ID Q6JB27 9VIRU PRELIMINARY; PRT; 735 AA.
AC Q6JB27
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VPI.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues." J. Virol. 78:6381-6388 (2004).
DR EMBL: AY510591; AA599276.1; -; Genomic_DNA.
DR SMR: Q6JB27; 217-735.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR001403; Parvo. Coat.
DR Pfam: PF00740; Parvo. coat; 1.
SQ SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A CRC64;
Query Match 87.1%; Score 2530.5; DB 2; Length 735;
Best Local Similarity 84.8%; Pred. No. 3.6e-176;
Matches 453; Conservative 35; Mismatches 45; Indels 1; Gaps 1;
QY 1 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTTALPTYNHLYKQISS 60
DB 203 MASGGGAPMADNNEGADGVGNASGNMHCDSQMLGDRVITTSRTTALPTYNHLYKQISS 262
QY 61 ASTGASNDNHYFGYSTPWCYFDNRFCHFSPRDMQRLINNNGRRPKRLNFKLFNIOVK 120
DB 263 QS-GASNDNHYFGYSTPWCYFDNRFCHFSPRDMQRLINNNGRRPKRLNFKLFNIOVK 321
QY 121 EYTNNDGTTTANNLTSTVQVFSDEYQLPYVLGSAHQGCLPPPADVFMIPQYGYLTIN 180
DB 322 EYTNNDGTTTANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPPADVFMIPQYGYLTIN 381
QY 181 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTFSYTEEVEVPHSSYASHQSGLDRLMPLIDQY 240
DB 382 NSGQAVGRSSFYCLEYFSPQMLRTGNNFQFSTYTEDVPHSSYASHQSGLDRLMPLIDQY 441
QY 241 LYYLNRTQNSGSAQNKDLLFSRGSFAGMSVQPKNMLPGPCYRQQRVSKTKTDNNNSNF 300
DB 442 LYYLNRTQNSGTLTQSRLLFSQAGPTNMSLQAKNMLPGPCYRQQRVSKTKTDNNNSNF 501
QY 301 WTGASKTNLNGRESIINPGTAMASHKDEDEKFFPMGSMVIFKESAGASNTALDNVMTD 360
DB 502 WTAAKTYHLNGRDSLVPNPGPAMASHKDEDEKFFPMHGNLLFGKGGTTASNAELDNVMTD 561
QY 361 DEEIKATNPVATERFGTVAVNFQSSSTDPAATGDVHAMGALPGMWQODRDVYLGQPIWAKI 420
DB 562 DEEIKATNPVATERFGTVAVNFQSSSTDPAATGDVHAMGALPGMWQODRDVYLGQPIWAKI 621
QY 421 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAFSAATKFASTIYQSTGQSV 480
DB 622 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAFSAATKFASTIYQSTGQSV 681
QY 481 IEMWLOKSKRMNPEVQYTSNTAKSANDFTVNNGLYTERPRIGTRYLTPL 534
DB 682 IEMWLOKSKRMNPEIQTYSNKNKSVNVDFTVNDNGVSEBRPIGTRYLTPL 735
RESULT 11
056139_VIRU PRELIMINARY; PRT; 736 AA.
ID 056139_VIRU PRELIMINARY; PRT; 736 AA.
AC 056139;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capaid protein VPI.
OS Adeno-associated virus 3B.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=68742;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98080418; PubMed=9420229;
RA Rutledge E.A., Halbert C.L., Russell D.W.;
RT "Infectious clones and vectors derived from adeno-associated virus
RT (AAV) serotypes other than AAV type 2.";
RT J. Virol. 72:309-319(1998).
DR EMBL: AF028705; AAB95452.1; -; Genomic_DNA.
DR SMR: 056139; 217-736.
DR GO: GO:0019028; C:viral capaid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo. coat.
DR Pfam: PF00740; Parvo. coat; 1.
SQ SEQUENCE 736 AA; 81906 MW; DD52331ADSF0D70F CRC64;
Query Match 87.1%; Score 2530; DB 2; Length 736;
Best Local Similarity 86.0%; Pred. No. 3.9e-176;

Matches 460; Conservative 27; Mismatches 46; Indels 2; Gaps 2;
QY 1 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTTALPTYNHLYKQISS 60
DB 203 MASGGGAPMADNNEGADGVGNASGNMHCDSQMLGDRVITTSRTTALPTYNHLYKQISS 262
QY 61 ASTGASNDNHYFGYSTPWCYFDNRFCHFSPRDMQRLINNNGRRPKRLNFKLFNIOVK 120
DB 263 QS-GASNDNHYFGYSTPWCYFDNRFCHFSPRDMQRLINNNGRRPKRLNFKLFNIOVK 321
QY 121 EYTNNDGTTTANNLTSTVQVFSDEYQLPYVLGSAHQGCLPPPADVFMIPQYGYLTIN 180
DB 322 EYTNNDGTTTANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPPADVFMIPQYGYLTIN 381
QY 181 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTFSYTEEVEVPHSSYASHQSGLDRLMPLIDQY 240
DB 382 NSGQAVGRSSFYCLEYFSPQMLRTGNNFQFSTYTEDVPHSSYASHQSGLDRLMPLIDQY 441
QY 241 LYYLNRTQNSGSAQNKDLLFSRGSFAGMSVQPKNMLPGPCYRQQRVSKTKTDNNNSNF 299
DB 442 LYYLNRTQNSGTLTQSRLLFSQAGPTNMSLQAKNMLPGPCYRQQRVSKTKTDNNNSNF 501
QY 300 WTGASKTNLNGRESIINPGTAMASHKDEDEKFFPMGSMVIFKESAGASNTALDNVMT 359
DB 502 WTAAKTYHLNGRDSLVPNPGPAMASHKDEDEKFFPMHGNLLFGKGGTTASNAELDNVMT 561
QY 360 DEEIKATNPVATERFGTVAVNFQSSSTDPAATGDVHAMGALPGMWQODRDVYLGQPIWAK 419
DB 562 DEEIKATNPVATERFGTVAVNFQSSSTDPAATGDVHAMGALPGMWQODRDVYLGQPIWAK 621
QY 420 IPTHGHPSPLMGFGGLKNPPQILIKNTVPANPPAFSAATKFASTIYQSTGQSV 479
DB 622 IPTHGHPSPLMGFGGLKNPPQILIKNTVPANPPAFSAATKFASTIYQSTGQSV 681
QY 480 IEMWLOKSKRMNPEVQYTSNTAKSANDFTVNNGLYTERPRIGTRYLTPL 534
DB 682 IEMWLOKSKRMNPEIQTYSNKNKSVNVDFTVNDNGVSEBRPIGTRYLTPL 736
RESULT 12
06JBZ1_VIRU PRELIMINARY; PRT; 735 AA.
ID 06JBZ1_VIRU PRELIMINARY; PRT; 735 AA.
AC 06JBZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capaid protein VPI.
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_Taxid=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvirra M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
RT tissues.";
RT J. Virol. 78:6381-6388(2004).
DR EMBL: AY530628; AAS99313.1; -; Genomic_DNA.
DR SMR: 06JBZ1; 217-735.
DR GO: GO:0019028; C:viral capaid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001403; Parvo. coat.
DR Pfam: PF00740; Parvo. coat; 1.
SQ SEQUENCE 735 AA; 81868 MW; 1654ED6287F5474 CRC64;
Query Match 87.0%; Score 2529.5; DB 2; Length 735;
Best Local Similarity 85.0%; Pred. No. 4.2e-176;
Matches 454; Conservative 34; Mismatches 45; Indels 1; Gaps 1;
QY 1 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTTALPTYNHLYKQISS 60

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Db      203 MATGSGAPMADNNEGADGVGNSGNMHCDSQMLGDRVITTTSTRTMALPTYNHLYKQISS 262
Qy      61 ASTGASNDNHYFGYSTPMWGFDFNRPFHCHFSPRDMQRLINNMGFRPKLNFKNLYOKV 120
Db      263 QS-GASNDNHYFGYSTPMWGFDFNRPFHCHFSPRDMQRLINNMGFRPKLNFKNLYOKV 321
Qy      121 EYTTNDGVTTIANNLITSTVOVFSDESEYOLPYVLGSAHQGLPPFPADVFMIPQYGYLTJLN 180
Db      322 EYTTNDGVTTIANNLITSTVOVFSDESEYOLPYVLGSAHQGLPPFPADVFMIPQYGYLTJLN 381
Qy      181 NSQAVGSSFFCYCLEYFSPQMLRTGNNTFFSYTFEEVPHSSYAHOSQSLDRMLNPLIDQY 240
Db      382 NSQAVGSSFFCYCLEYFSPQMLRTGNNTFFSYTFEEVPHSSYAHOSQSLDRMLNPLIDQY 441
Qy      241 LYTLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMLPGPCYRQORVSKTTDNNNSNF 300
Db      442 LYTLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMLPGPCYRQORVSKTTDNNNSNF 501
Qy      301 WTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FQKESAGASNTALDNVMTD 360
Db      502 WTAAATKYHLNGRDSLVPNPGPAMASHKDEDEKFPMSGVMI FQKQGTNADADLDNVMITD 561
Qy      361 EERIKAATNPVATERTGTVAVNFGSSSTDPATGVDYAHMAGALPGMWQDRDVLVLOGPIMAKI 420
Db      562 EERIKAATNPVATERTGTVAVNFGSSSTDPATGVDYAHMAGALPGMWQDRDVLVLOGPIMAKI 621
Qy      421 PHTDGHFHPSPMLMGFGGLKPNPQILIKNTVPANPPAEFSATKFASTTOYSTQGVSV 480
Db      622 PHTDGHFHPSPMLMGFGGLKPNPQILIKNTVPANPPAEFSATKFASTTOYSTQGVSV 681
Qy      481 IEWELQKENSKRNPVEVQYTSNYAKSANDFTVNDNGLYTEPRPIGRYLTIRPL 534
Db      682 IEWELQKENSKRNPVEVQYTSNYAKSANDFTVNDNGLYTEPRPIGRYLTIRPL 735

RESULT 13
ID 065311.9VIRU PRELIMINARY; PRT; 736 AA.
AC 065311.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein.
OS Adeno-associated virus 3.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=46350;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3H;
RX MEDLINE=96266430; PubMed=8661429; DOI=10.1006/viro.1996.0367;
RA Muramatsu S., Mizukami H., Young N.S., Brown K.B.;
RT "Nucleotide sequencing and generation of an infectious clone of adeno-
associated virus 3.";
RL Virology 221:208-217(1996).
DR EMBL; U48704; AAC55049.1; -; Genomic_DNA.
DR SMR; Q65311; 217-736.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 736 AA; 81660 MW; AFLEF47B5C67A10 CRC64;

Query Match 87.0%; Score 2528; DB 2; Length 736;
Best Local Similarity 85.8%; Pred. No. 5.5e-176;
Matches 453; Conservative 28; Mismatches 46; Indels 2; Gaps 2;

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Qy      121 EYTTNDGVTTIANNLITSTVOVFSDESEYOLPYVLGSAHQGLPPFPADVFMIPQYGYLTJLN 180
Db      322 EYTTNDGVTTIANNLITSTVOVFSDESEYOLPYVLGSAHQGLPPFPADVFMIPQYGYLTJLN 381
Qy      181 NSQAVGSSFFCYCLEYFSPQMLRTGNNTFFSYTFEEVPHSSYAHOSQSLDRMLNPLIDQY 240
Db      382 NSQAVGSSFFCYCLEYFSPQMLRTGNNTFFSYTFEEVPHSSYAHOSQSLDRMLNPLIDQY 441
Qy      241 LYTLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMLPGPCYRQORVSKTTDNNNSNF 299
Db      442 LYTLNRTOQSGSAQNKDLLFSRGSFAGMSVQPKMLPGPCYRQORVSKTTDNNNSNF 501
Qy      300 TWTGASKYNLNGRESIINPGTAMASHKDEDEKFPMSGVMI FQKESAGASNTALDNVMT 359
Db      502 PWTAAASKYHLNGRDSLVPNPGPAMASHKDEDEKFPMSGVMI FQKQGTNADADLDNVMIT 561
Qy      360 DEERIKAATNPVATERTGTVAVNFGSSSTDPATGVDYAHMAGALPGMWQDRDVLVLOGPIMAKI 419
Db      562 DEERIKAATNPVATERTGTVAVNFGSSSTDPATGVDYAHMAGALPGMWQDRDVLVLOGPIMAKI 621
Qy      420 IPHTDGHFHPSPMLMGFGGLKPNPQILIKNTVPANPPAEFSATKFASTTOYSTQGVSV 479
Db      622 IPHTDGHFHPSPMLMGFGGLKPNPQILIKNTVPANPPAEFSATKFASTTOYSTQGVSV 681
Qy      480 IEWELQKENSKRNPVEVQYTSNYAKSANDFTVNDNGLYTEPRPIGRYLTIRPL 534
Db      682 IEWELQKENSKRNPVEVQYTSNYAKSANDFTVNDNGLYTEPRPIGRYLTIRPL 736

RESULT 14
ID 06JC38.9VIRU PRELIMINARY; PRT; 735 AA.
AC 06JC38.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein VPI.
GN Name=cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alvirra M.R., Lu Y., Calcedo R., Zhou X.,
RA Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
tissues.";
RL J. Virol. 78:6381-6388(2004).
DR EMBL; AY530581; AAS99266.1; -; Genomic_DNA.
DR SMR; 06JC38; 217-735.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
SQ SEQUENCE 735 AA; 81913 MW; 58131PDAEB024251 CRC64;

Query Match 86.9%; Score 2524.5; DB 2; Length 735;
Best Local Similarity 84.8%; Pred. No. 9.8e-176;
Matches 453; Conservative 34; Mismatches 46; Indels 1; Gaps 1;

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OY 181 NSGQAVGRSSFYCLEYFPSSOMLRTGNNTFSTYFEFVPHSHSYAHSSQSLDRMLNPLIDY 240
DB 382 NSGQAVGRSSFYCLEYFPSSOMLRTGNNTFSTYFEFVPHSHSYAHSSQSLDRMLNPLIDY 441
OY 241 LYYLNRTONOGSGAONKDLFSRGSFAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
DB 442 LYYLNRTONOGSGTLLQOSRLLFSQAGPFTSMISLQAKNMLPQPCYRQORVSKTKTDNNNSNFT 501
OY 301 WTGASKYNLNGRESIIINFGTAMASHKODEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 360
DB 502 WTAAATKYNLNGRDSLVNPGPAMASHKODEDEKFFPMHGTLLIFGKQGTNANDADLDHVMITD 561
OY 421 EEEIKATNPVATERFGTAVAVNFSSSTDPAATGDVAMGALPGMWQDRDVTLLQGPIMAKI 420
DB 562 EEEIKATNPVATERFGTAVAVNFSSSTDPAATGDVAMGALPGMWQDRDVTLLQGPIMAKI 621
OY 421 PHTDGHFHPSPLMGFGGLKPNPPQILIKNTVPANPAPAFSATKFASTITQYSTGQSV 480
DB 622 PHTDGHFHPSPLMGFGGLKPNPPQILIKNTVPANPAPAFSATKFASTITQYSTGQSV 681
OY 481 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNGLYTERPRIGTRYLTRPL 534
DB 682 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNGLYTERPRIGTRYLTRPL 735

RESULT 15
O6JC42_9VIRU PRELIMINARY; PRT; 735 AA.
AC O6JC42;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Capsid protein VP1.
GN Name=caps;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
OX NCBI_TaxID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
RA Gao G., Vandenberghe L.H., Alviria M.R., Lu Y., Calcedo R., Zhou X.,
  Wilson J.M.;
RT "Clades of Adeno-associated viruses are widely disseminated in human
  tissues.";
RU J. Virol. 78:6381-6388(2004).
DR EMBL; AY530577; AAS99262.1; -, Genomic_DNA.
DR SMR; Q6JC42; 217-735.
DR GO; GO:0019028; C:Viral capsid; IBA.
DR GO; GO:0005198; F:structural molecule activity; IBA.
DR InterPro; IPR001403; Parvo coat.
DR Pfam; PF00740; Parvo coat; 1.
SQ SEQUENCE 735 AA; 82114 MM; 598748255744D5FB CRC64;

Query Match 86.9%; Score 2524.5; DB 2; Length 735;
Best Local Similarity 84.8%; Pred. No. 9.8e-176;
Matches 453; Conservative 35; Mismatches 45; Indels 1; Gaps 1;

OY 1 MASGGAPPADNNEGADGVGNASGNWCHDSTWLGDRVITTSRTYMAALPTYNHLYKOISS 60
DB 203 MATGSGAPPADNNEGADGVGNSSGNWCHDSTWLGDRVITTSRTYMAALPTYNHLYKOISS 262
OY 61 ASTGASNDNHFGYSTPQWYFPDPRPHCHFSPPDQRLINNMMGFRPKLNFQIYQK 120
DB 263 QG-GASNDNHFGYSTPQWYFPDPRPHCHFSPPDQRLINNMMGFRPKLNFQIYQK 321
OY 121 EYTTNDGVTITIANNLSTVQVSDSEYQIPYVLGSAHQCLPPPADVPMIPOYGYITLN 180
DB 322 EYTTNDGVTITIANNLSTVQVFTDSYQIPYVLGSAHQCLPPPADVPMIPOYGYITLN 381
OY 181 NSGQAVGRSSFYCLEYFPSSOMLRTGNNTFSTYFEFVPHSHSYAHSSQSLDRMLNPLIDY 240
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OY 241 LYYLNRTONOGSGAONKDLFSRGSFAGMSVQPKMWLPQPCYRQORVSKTKTDNNNSNFT 300
DB 442 LYYLNRTONOGSGTLLQOSRLLFSQAGPFTSMISLQAKNMLPQPCYRQORVSKTKTDNNNSNFT 501
OY 301 WTGASKYNLNGRESIIINFGTAMASHKODEDEKFFPMGSMVIFGKESAGASNTALDNVMTD 360
DB 502 WTAAATKYNLNGRDSLVNPGPAMASHKODEDEKFFPMHGTLLIFGKQGTNANDADLDHVMITD 561
OY 361 EEEIKATNPVATERFGTAVAVNFSSSTDPAATGDVAMGALPGMWQDRDVTLLQGPIMAKI 420
DB 562 EEEIKATNPVATERFGTAVAVNFSSSTDPAATGDVAMGALPGMWQDRDVTLLQGPIMAKI 621
OY 421 PHTDGHFHPSPLMGFGGLKPNPPQILIKNTVPANPAPAFSATKFASTITQYSTGQSV 480
DB 622 PHTDGHFHPSPLMGFGGLKPNPPQILIKNTVPANPAPAFSATKFASTITQYSTGQSV 681
OY 481 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNGLYTERPRIGTRYLTRPL 534
DB 682 IEMELQKNSKRMNPEVOYTSNYAKSANDFTVDNGLYTERPRIGTRYLTRPL 735
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Search completed: November 23, 2005, 17:41:20
Job time : 104.857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 17:26:29 ; Search time 24.2857 Seconds
(without alignments)
1817.892 Million cell updates/sec

Title: US-10-696-282-17

Perfect score: 2906
Sequence: 1 MASGGGAPMADNNEGADGVG.....NNGLYTEPRPIGTIRYLRPL 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seque, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/aa/5.COMB.pep: *
2: /cgn2_6/prodata/1/aa/6.COMB.pep: *
3: /cgn2_6/prodata/1/aa/H.COMB.pep: *
4: /cgn2_6/prodata/1/aa/PCTUS.COMB.pep: *
5: /cgn2_6/prodata/1/aa/RE.COMB.pep: *
6: /cgn2_6/prodata/1/aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2906	100.0	534	2	US-09-807-802A-17
2	2906	100.0	534	2	US-09-807-802A-15
3	2906	100.0	736	2	US-09-807-802A-3
4	2906	100.0	736	2	US-09-807-802A-13
5	2481.5	85.4	533	2	US-10-038-972A-15
6	2481.5	85.4	533	2	US-10-038-972A-14
7	2481.5	85.4	735	2	US-09-321-589-1
8	2481.5	85.4	735	2	US-10-293-478-1
9	2481.5	85.4	735	2	US-10-038-972A-13
10	1690.5	58.2	544	2	US-09-532-594B-18
11	1690.5	58.2	544	2	US-09-532-594B-16
12	1690.5	58.2	734	2	US-09-532-594B-4
13	1665	57.3	532	2	US-09-533-427-6
14	1665	57.3	532	2	US-09-533-427-5
15	1665	57.3	724	2	US-09-533-427-4
16	491.5	16.9	756	2	US-09-438-268-4
17	486	16.7	554	2	US-10-187-253E-29
18	486	16.7	554	2	US-10-187-253E-35
19	486	16.7	781	2	US-10-187-253E-27
20	479.5	16.5	543	2	US-08-856-841-22
21	477	16.4	781	2	US-10-187-253E-33
22	326	11.2	415	2	US-08-856-841-20
23	318	10.9	395	2	US-08-856-841-13
24	318	10.9	486	2	US-08-856-841-19
25	317.5	10.9	500	2	US-08-856-841-16
26	317.5	10.9	501	2	US-08-856-841-18
27	304.5	10.5	264	2	US-08-856-841-14

28	303	10.4	398	2	US-08-856-841-21	Sequence 21, App1
29	209.5	7.2	579	6	5223424-13	Patent No. 5223424
30	183	6.3	584	2	US-09-022-949-2	Sequence 17, App1
31	171	5.9	387	2	US-08-856-841-17	Sequence 4, App1
32	132.5	4.6	489	2	US-10-376-397B-4	Sequence 3855, Ap
33	119	4.1	1095	2	US-09-107-532A-3855	Sequence 23413, A
34	111.5	3.8	551	2	US-09-248-796A-23413	Sequence 27, App1
35	111	3.8	655	1	US-08-469-202-27	Sequence 34, App1
36	111	3.8	655	1	US-08-484-434C-34	Sequence 34, App1
37	111	3.8	655	2	US-09-384-361-34	Sequence 4, App1
38	109	3.8	1186	1	US-08-485-568A-4	Sequence 6, App1
39	109	3.8	1186	1	US-08-357-698-6	Sequence 6, App1
40	109	3.8	1186	1	US-08-590-554A-4	Sequence 4, App1
41	109	3.8	1186	1	US-09-184-223-4	Sequence 6, App1
42	109	3.8	1186	4	PCT-US93-12682-6	Sequence 14, App1
43	108.5	3.7	1637	2	US-10-172-502-14	Sequence 78, App1
44	108	3.7	624	2	US-08-947-965-78	Sequence 28, App1
45	108	3.7	655	1	US-08-469-202-28	

ALIGNMENTS

RESULT 1									
US-09-807-802A-17									
Sequence 17, Application US/09807802A									
Patent No. 6759237									
GENERAL INFORMATION:									
APPLICANT: Xiao, Weidong									
APPLICANT: Wilson, James M.									
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences.									
FILE REFERENCE: GNVN.031USA									
CURRENT APPLICATION NUMBER: US/09/807,802A									
CURRENT FILING DATE: 2002-02-21									
PRIOR APPLICATION NUMBER: US 60/107,114									
PRIOR FILING DATE: 1998-11-05									
PRIOR APPLICATION NUMBER: PCT/US99/25694									
PRIOR FILING DATE: 1999-11-02									
NUMBER OF SEQ ID NOS: 20									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 17									
LENGTH: 534									
TYPE: PRT									
ORGANISM: AAV-1									
US-09-807-802A-17									
Query Match									
Best Local Similarity 100.0%; Score 2906; DB 2; Length 534;									
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MASGGGAPMADNNEGADGVGNASGNMHCSTWLGDRVITTSRTTMA	PTNNHL	YKQISS	60				
QY	61	ASTGASNDNHFFCYSTPMGYPFNRPHCHPSPRDMQRL	INNKGFPKRLNFKL	ENIYQK	120				
DB	61	ASTGASNDNHFFCYSTPMGYPFNRPHCHPSPRDMQRL	INNKGFPKRLNFKL	ENIYQK	120				
QY	121	EVTNDNGVTTIANNLSTQVFSDSRYQLPYVIGSAHQCL	PPPADVPMI	POYGVLTN	180				
DB	121	EVTNDNGVTTIANNLSTQVFSDSRYQLPYVIGSAHQCL	PPPADVPMI	POYGVLTN	180				
QY	181	NGSOAVGRSSPYCLEYFSPQMLRTGNNFTFSYTFE	VPFHSSYAHSQSL	DLRLANPLIDY	240				
DB	181	NGSOAVGRSSPYCLEYFSPQMLRTGNNFTFSYTFE	VPFHSSYAHSQSL	DLRLANPLIDY	240				
QY	241	LYTLNFTONQSGAOKKDLLFSRGSFAGMSVOPKMW	PGPCYRQOVS	KTKTDNNNSFT	300				
DB	241	LYTLNFTONQSGAOKKDLLFSRGSFAGMSVOPKMW	PGPCYRQOVS	KTKTDNNNSFT	300				
QY	301	WTGASVYNLNGRESIINPGTAMASHKDDKXFP	PMGSMWIFGKES	AGASNTALDNWITD	360				
DB	301	WTGASVYNLNGRESIINPGTAMASHKDDKXFP	PMGSMWIFGKES	AGASNTALDNWITD	360				

Db 301 WTGASKYVNLNGRESIIINPGTAMASHKDEDEKFFPMGSGVMI FGKESAGASNTALDVMITD 360
Qy 361 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 420
Db 361 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 420
Qy 421 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 480
Db 421 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 480
Qy 481 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534
Db 481 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534

RESULT 2

US-09-807-802A-15
; Sequence 15, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNVN.03USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-15

Query Match 100.0%; Score 2906; DB 2; Length 599;

Best Local Similarity 100.0%; Pred. No. 1,1e-257;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTMALPTYNHLYKQISS 60
Db 66 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTMALPTYNHLYKQISS 125
Qy 61 ASTGASNDNHFGYSTPMGYDFNRPCHFSPRDMQRLINNMGFRPKLNFKLFNIQVK 120
Db 126 ASTGASNDNHFGYSTPMGYDFNRPCHFSPRDMQRLINNMGFRPKLNFKLFNIQVK 185
Qy 121 EYTTNDGVTITANNLTSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTIN 180
Db 186 EYTTNDGVTITANNLTSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTIN 245
Qy 181 NSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFEVPHSSVAHSQSLDRLMNPIDY 240
Db 246 NSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFEVPHSSVAHSQSLDRLMNPIDY 305
Qy 241 LYYLNRTONQSGAQNKDILFSRGSFAGMSVQPKNMLPGPCYRQORVSKTTDNNNSFT 300
Db 306 LYYLNRTONQSGAQNKDILFSRGSFAGMSVQPKNMLPGPCYRQORVSKTTDNNNSFT 365
Qy 301 WTGASKYVNLNGRESIIINPGTAMASHKDEDEKFFPMGSGVMI FGKESAGASNTALDVMITD 360
Db 366 WTGASKYVNLNGRESIIINPGTAMASHKDEDEKFFPMGSGVMI FGKESAGASNTALDVMITD 425
Qy 361 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 420
Db 426 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 485
Qy 421 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 480

Db 486 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 545
Qy 481 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534
Db 546 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 599

RESULT 3

US-09-807-802A-3
; Sequence 3, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; FILE REFERENCE: GNVN.03USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-3

Query Match 100.0%; Score 2906; DB 2; Length 736;

Best Local Similarity 100.0%; Pred. No. 1,6e-257;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTMALPTYNHLYKQISS 60
Db 203 MASGGGAPMADNNEGADGVGNASGNMHCDSITWLGDRVITTSRTMALPTYNHLYKQISS 262
Qy 61 ASTGASNDNHFGYSTPMGYDFNRPCHFSPRDMQRLINNMGFRPKLNFKLFNIQVK 120
Db 263 ASTGASNDNHFGYSTPMGYDFNRPCHFSPRDMQRLINNMGFRPKLNFKLFNIQVK 322
Qy 121 EYTTNDGVTITANNLTSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTIN 180
Db 323 EYTTNDGVTITANNLTSTVQVFSDEYQLPYVLGSAHQCLPPPADVFMIPQYGYLTIN 382
Qy 181 NSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFEVPHSSVAHSQSLDRLMNPIDY 240
Db 383 NSQAVGRSSFYCLEYFSPQMLRTGNFTFSTFEVPHSSVAHSQSLDRLMNPIDY 442
Qy 241 LYYLNRTONQSGAQNKDILFSRGSFAGMSVQPKNMLPGPCYRQORVSKTTDNNNSFT 300
Db 443 LYYLNRTONQSGAQNKDILFSRGSFAGMSVQPKNMLPGPCYRQORVSKTTDNNNSFT 502
Qy 301 WTGASKYVNLNGRESIIINPGTAMASHKDEDEKFFPMGSGVMI FGKESAGASNTALDVMITD 360
Db 503 WTGASKYVNLNGRESIIINPGTAMASHKDEDEKFFPMGSGVMI FGKESAGASNTALDVMITD 562
Qy 361 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 420
Db 563 EEEIKATNPVATERGCTVAVNFQSSSTDPATGADVAMGALPGMWQODDVIYLGPIWAKI 622
Qy 421 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 480
Db 623 PHTDGHFHPSPLMGFGGLKNPPQILIKNTVPANPPAEFSATKFASTITQYSTQGVSE 682
Qy 481 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 534
Db 683 IEMELOKENSKRMNPEVOYTSNYAKSANVDFTVNNGLYTEBRPIGTRYLTRPL 736

RESULT 4


```
US-09-807-802A-13
; Sequence 13, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,
; FILE REFERENCE: GNPV.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-13

Query Match      100.0%; Score 2906; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.6e-257;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITTSRTWALPTYNNHLYKQISS 60
DB      203 MASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITTSRTWALPTYNNHLYKQISS 262
QY      61 ASTGASNDNHYFGYSTPMWGYFDNRFCHFSPPRDWQRLINNNGFPRKRLNFKLFNIQVK 120
DB      263 ASTGASNDNHYFGYSTPMWGYFDNRFCHFSPPRDWQRLINNNGFPRKRLNFKLFNIQVK 322
QY      121 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPQGYLTIN 180
DB      323 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPQGYLTIN 382
QY      181 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTSYTPEEVPFHSSVYAHOSQSLDRMLNPLIDQY 240
DB      383 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTSYTPEEVPFHSSVYAHOSQSLDRMLNPLIDQY 442
QY      241 LYYLNRTONQSGSAQNKDLLFSRGSPPAGMSVQPKMLPQPCYRQOVSKTKTDNNNSNFT 300
DB      443 LYYLNRTONQSGSAQNKDLLFSRGSPPAGMSVQPKMLPQPCYRQOVSKTKTDNNNSNFT 502
QY      301 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMSCVMI FGKESAGASTALDNYMITD 360
DB      503 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMSCVMI FGKESAGASTALDNYMITD 562
QY      361 EEEIKATNPVATERFGTVAANFOSSSTDPATGVDHAMGALPGMWODRDVYLOGPIWAKI 420
DB      563 EEEIKATNPVATERFGTVAANFOSSSTDPATGVDHAMGALPGMWODRDVYLOGPIWAKI 622
QY      421 PHTDGHFHPSPLMGGFGLKNPPOILLIKNTVPANPAEFSATKFASTIQTSTGVSV 480
DB      623 PHTDGHFHPSPLMGGFGLKNPPOILLIKNTVPANPAEFSATKFASTIQTSTGVSV 682
QY      481 IEWELQKENSKRNPVEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB      683 IEWELQKENSKRNPVEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736

RESULT 5
US-10-038-972A-15
; Sequence 15, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038, 972A
```

```
CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 533
; TYPE: PRT
; ORGANISM: adeno-associated virus 2 VP3 capsid protien
US-10-038-972A-15

Query Match      85.4%; Score 2481.5; DB 2; Length 533;
Best Local Similarity 83.3%; Pred. No. 8.3e-219;
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1;

QY      1 MASGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITTSRTWALPTYNNHLYKQISS 60
DB      1 MATGGGAPMADNNEGADGVGNASGNWCHDSTWLGDRVITTSRTWALPTYNNHLYKQISS 60
QY      61 ASTGASNDNHYFGYSTPMWGYFDNRFCHFSPPRDWQRLINNNGFPRKRLNFKLFNIQVK 120
DB      61 Q8-GASNDNHYFGYSTPMWGYFDNRFCHFSPPRDWQRLINNNGFPRKRLNFKLFNIQVK 119
QY      121 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPQGYLTIN 180
DB      120 EVTTNDGVTITANNLITSTVOVFSDEYQLPYVLGSAHQCLPPPADVFMIPQGYLTIN 179
QY      181 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTSYTPEEVPFHSSVYAHOSQSLDRMLNPLIDQY 240
DB      180 NSGQAVGRSSFYCLEYFSPQMLRTGNNFTSYTPEEVPFHSSVYAHOSQSLDRMLNPLIDQY 239
QY      241 LYYLNRTONQSGSAQNKDLLFSRGSPPAGMSVQPKMLPQPCYRQOVSKTKTDNNNSNFT 300
DB      240 LYYLNRTONQSGSAQNKDLLFSRGSPPAGMSVQPKMLPQPCYRQOVSKTKTDNNNSNFT 299
QY      301 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMSCVMI FGKESAGASTALDNYMITD 360
DB      300 WTGASKYNLNGRESIINPGTAMASHKODEKFFPMSCVMI FGKESAGASTALDNYMITD 359
QY      361 EEEIKATNPVATERFGTVAANFOSSSTDPATGVDHAMGALPGMWODRDVYLOGPIWAKI 420
DB      360 EEEIKATNPVATERFGTVAANFOSSSTDPATGVDHAMGALPGMWODRDVYLOGPIWAKI 419
QY      421 PHTDGHFHPSPLMGGFGLKNPPOILLIKNTVPANPAEFSATKFASTIQTSTGVSV 480
DB      420 PHTDGHFHPSPLMGGFGLKNPPOILLIKNTVPANPAEFSATKFASTIQTSTGVSV 479
QY      481 IEWELQKENSKRNPVEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 534
DB      480 IEWELQKENSKRNPVEVOYTSNVAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 533

RESULT 6
US-10-038-972A-14
; Sequence 14, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038, 972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 598
; TYPE: PRT
; ORGANISM: adeno-associated virus 2 VP2 capsid protien
US-10-038-972A-14

Query Match      85.4%; Score 2481.5; DB 2; Length 598;
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Best Local Similarity 83.3%; Pred. No. 9.9e-219;
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1;

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QY 1 MASGGAPMADNNEGADGVGNASGNMHCDSITWLDGRIVITTSRTTALPTYNHLYKQISS 60
DB 66 MATGSGAPMADNNEGADGVGNASGNMHCDSITWMDGRIVITTSRTTALPTYNHLYKQISS 125
QY 61 ASTGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 120
DB 126 QGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 184
QY 121 EVTTNDGVTIANNTLSTVQVFSDEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 180
DB 185 EYTONDGTITIANNTLSTVQVFTDSEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 244
QY 181 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 240
DB 245 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 304
QY 241 LYYLNRTONOGSGAONKDLFSGRSPAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSFT 300
DB 305 LYYLSRTNTPSGTTTQSRLOFQAGASDIRDQSRMWLPQPCYRQORVSKTSADNNSEYS 364
QY 301 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASNTALDNVMTD 360
DB 365 WTGATKYHLNGRDSLVPNGPAMASHKDEDEKFFQSGVLIFFGQSKSEKTNVDIEKWMITD 424
QY 361 EEEIKATNPVATERGCTVAVNFOSSSTDPAITGDVHAMALPGMWODRDVYLQGPIMAKI 420
DB 425 EEEIRTNPVATEBGYSVTNLQGRNQATADVNTOGVLPGMWODRDVYLQGPIMAKI 484
QY 421 PHTDGHFSPPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSFTQYSTGVSE 480
DB 485 PHTDGHFSPPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSFTQYSTGVSE 544
QY 481 IEMELQENSKRMNPEVQYTSNVAKSANDFTVNNGLYTEPRIGTRYLTRPL 534
DB 545 IEMELQENSKRMNPEIQYTSNVAKSANDFTVNTGVSEPRIGTRYLTRNL 598

RESULT 7
US-09-321-589-1
; Sequence 1, Application US/09321589
; Patent No. 6498244
; GENERAL INFORMATION:
; APPLICANT: PATEL, SATIL D.
; APPLICANT: MCARTHUR, JAMES G.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/09/321,589
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Adeno-associated virus
US-09-321-589-1
```

Query Match 85.4%; Score 2481.5; DB 2; Length 735;
Best Local Similarity 83.3%; Pred. No. 1.4e-218;
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1;

```
QY 1 MASGGAPMADNNEGADGVGNASGNMHCDSITWLDGRIVITTSRTTALPTYNHLYKQISS 60
DB 203 MATGSGAPMADNNEGADGVGNASGNMHCDSITWMDGRIVITTSRTTALPTYNHLYKQISS 262
QY 61 ASTGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 120
DB 263 QGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 321
QY 121 EVTTNDGVTIANNTLSTVQVFSDEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 180
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DB 322 EYTONDGTITIANNTLSTVQVFTDSEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 381
QY 181 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 240
DB 382 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 441
QY 241 LYYLNRTONOGSGAONKDLFSGRSPAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSFT 300
DB 442 LYYLSRTNTPSGTTTQSRLOFQAGASDIRDQSRMWLPQPCYRQORVSKTSADNNSEYS 501
QY 301 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASNTALDNVMTD 360
DB 502 WTGATKYHLNGRDSLVPNGPAMASHKDEDEKFFQSGVLIFFGQSKSEKTNVDIEKWMITD 561
QY 361 EEEIKATNPVATERGCTVAVNFOSSSTDPAITGDVHAMALPGMWODRDVYLQGPIMAKI 420
DB 562 EEEIRTNPVATEBGYSVTNLQGRNQATADVNTOGVLPGMWODRDVYLQGPIMAKI 621
QY 421 PHTDGHFSPPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSFTQYSTGVSE 480
DB 622 PHTDGHFSPPLMGFGFLKNPPQILIKNTVPANPAPAEFSATKFSFTQYSTGVSE 681
QY 481 IEMELQENSKRMNPEVQYTSNVAKSANDFTVNNGLYTEPRIGTRYLTRPL 534
DB 682 IEMELQENSKRMNPEIQYTSNVAKSANDFTVNTGVSEPRIGTRYLTRNL 735
```

```
RESULT 8
US-10-293-478-1
; Sequence 1, Application US/10293478
; Patent No. 6733757
; GENERAL INFORMATION:
; APPLICANT: PATEL, SATIL D.
; APPLICANT: MCARTHUR, JAMES G.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/10/293,478
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/321,589
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Adeno-associated virus
US-10-293-478-1
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Query Match 85.4%; Score 2481.5; DB 2; Length 735;
Best Local Similarity 83.3%; Pred. No. 1.4e-218;
Matches 445; Conservative 37; Mismatches 51; Indels 1; Gaps 1;

```
QY 1 MASGGAPMADNNEGADGVGNASGNMHCDSITWLDGRIVITTSRTTALPTYNHLYKQISS 60
DB 203 MATGSGAPMADNNEGADGVGNASGNMHCDSITWMDGRIVITTSRTTALPTYNHLYKQISS 262
QY 61 ASTGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 120
DB 263 QGASNDNHFGYSTPWCYFDNFRFCHFSFPRDQRLINNMGFPRKLNFKLFNIQVK 321
QY 121 EVTTNDGVTIANNTLSTVQVFSDEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 180
DB 322 EYTONDGTITIANNTLSTVQVFTDSEYQLPYVLGSAHQGLPPPADVFMIPQYGYLTLN 381
QY 181 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 240
DB 382 NGSQAVGRSSFYCLEYFPSSQMLRTGNNTFTSYTEEDVPFHSSYAHQSGLDRMLNPLIDQY 441
QY 241 LYYLNRTONOGSGAONKDLFSGRSPAGMSVOPKMWLPQPCYRQORVSKTKTDNNNSFT 300
DB 442 LYYLSRTNTPSGTTTQSRLOFQAGASDIRDQSRMWLPQPCYRQORVSKTSADNNSEYS 501
QY 301 WTGASKYNIINGRESIINPGTAMASHKDEDEKFFPMGCVMTFGKESAGASNTALDNVMTD 360
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RESULT 11
US-09-532-594B-16

```

: Sequence 6 Application US/095333427
: Patent No. 6855314
: GENERAL INFORMATION:
: APPLICANT: Chlorini, John
: APPLICANT: Kotlin, Robert M.
: APPLICANT: Safer, Brian
: APPLICANT: Davidson, Elizabeth
: APPLICANT: Zahner, Joseph
: TITLE OF INVENTION: JAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
: FILE REFERENCE: 14014.0323U2
: CURRENT APPLICATION NUMBER: US/09/533,427
: CURRENT FILING DATE: 2000-03-22
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 532
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e =
: OTHER INFORMATION: Synthetic construct
: US-09-533-427-6

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	Query Match	Similarity	57.3%	Score 1665	DB 2	Length 532	
	Best Local	Similarity	58.9%	Pred. No. 6-5e-144			
	Matches	318	Conservative	54	Mismatches 154	Indels 14	Gaps 5
Qy	1	MASGGGADPMADNNBEGADGVNAGSAGNMHCDSTWLGDRVITTSRTYMALPTYNHNLKYQIIS	60				
Db	1	MSAGGGGELGANNQCADGVNAGSGMHCDSTWMGDRVVTKSTRYTWLSPSYNNHGYREIKS	60				
Qy	61	ASTAGSNNNHFCVSTPMGYPDPFNK FCHQFSPRDMQRLINNMGFRPKLNKLENIQVK	120				
Db	61	GSVDSSNANNAFYGSTPMWGFDPFNK FSHMSRDRDQRLINNMGFRPSLRKXKLNIOVK	120				
Qy	121	EYTTNDGYTTIANNLSTVOVPSDSEYQLPYVLGSAHQGLPFPADVFPMI.PQYGYLTN	180				
Db	121	EYTVQDSTTTIANNLSTVOVFTDDYQLPYVVGNGTEGCLPAPFPQVFTLLPQGYATLN	180				
Qy	181	--NSGQAVGRSSFFCLLEYFPSPQMLRTGNNFTTSYFEEVYFPHSSVAHSGSLDRMLNPLID	238				
Db	181	RDNTNPTPERSFFCLLEYFPSPQMLRTGNNFEFTYNEEVPFPHSSAPASQNLKLANPLVD	240				
Qy	239	OYLYYLNTFONSGSAGNNDLLEFRSGSPAGMSVQP-KXMLPPPCRCROGVSRTKTDNNNS	297				
Db	241	QYLYFVSTNTNGCYQVFNKL-----AGRYANTYKMFPPPMGRTQGMNIGSGVNRS	293				
Qy	298	NETTWGASKYNLNGRESIINPQTAMASHKDEDEKFFPMSGVMI.FGKESAGASNTAL--D	354				
Db	294	VSAPFTTRMELEGASVYQVPPQNGMTNNLQGSNTYVALENTWIFNSQNPANPGTATYLEG	353				
Qy	335	NVMTIDEEIKATNPVATYRFGTVAVNPFSSSTDPATGTVHAMGLPGVMWDDPQVYLOG	414				
Db	354	NMLITSESTQGVNVAVYVVGQMAITNNSSTTAPATGYTNLQEIIVPGSWMERDVIYLOG	413				
Qy	415	PIMAKIPHTDGFPHSPPLMGFGFLKNPPOQLIKTTPVANPAPAESATKFPASFITYOST	474				
Db	414	PIMAKIPETGALFPHSPAMGFGFLGNPPEMMLIKTTPVGN-ITSSDVVPVSSFITYOST	472				
Qy	475	GOVSVEIEMELQKENSKRNPFEVQYTSNYAKASANDFTVDDNGLYTEPPDIGRILYLRPL	534				
Db	473	GOVTBEMEMELKKENSKRNPETQYNNYNDQFVDFAPDSTGGEYKTRTPIGRILYLRPL	532				

```

1  APPLICANT: Zabner, Joseph
2  TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
3  FILE REFERENCE: 14014.032302
4  CURRENT APPLICATION NUMBER: US/09/533,427
5  CURRENT FILING DATE: 2000-03-22
6  NUMBER OF SEQ ID NOS: 23
7  SOFTWARE: FastSeq for Windows Version 3.0
8  SEQ ID NO 5
9  LENGTH: 588
10 TYPE: PRT
11 ORGANISM: Artificial Sequence
12 FEATURE:
13 OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e =
14 OTHER INFORMATION: synthetic construct
15 US-09-533-427-5

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```

Query Match 57.3%; Score 1665; DB 2; Length 588;
Best Local Similarity 58.9%; Pred. No. 7.6e-144;
Matches 318; Conservative 54; Mismatches 154; Indels 14; Gaps 5;

QY      1 MASGGAPPMADNNEGADGVGNAGSNMHCSTWLCDRVITTTSTRTWALPTYNHLYKQISS 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      57 MSAGGGPPLGDNNGAGDGVGNASGDWCHDSTWMDGRVVTYKSTRTWVLPSTYNNHOREKIS 116
QY      61 ASTGASDNHYEGYSTWGYFDENRFHCSPRPMOGLINNMGFRPRLFLFKFNIOVK 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      117 GSVDSNANAPFGYSTWGYFDENRFHSHSFRMOMLNNYWFRRPSRLAKFNIOVK 176
QY      121 EVTTNDGVTITANNLSTVQYFSDSEYQLPYLGSAHQCLPPPADVFMIPQGYTLTN 180
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      177 EVTVQDSTTTIANLNLSTVQYFVTDYQLPVVNGNTEGCLPAPPQVFTLPQGYATLN 236
QY      181 --NGSQAVRGSFYCLLEYFSPQMTRTGNNTFFSTFEEVPRPHSSYAHQSQDLRLNPLD 238
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      237 RDNTEENPTERSFCLEYFSPKMLRTGNNEFFTYFEEVPRHSSFAPSQNLFKLANPLVD 296
QY      239 QYLTYLRNTQOSSAQNKDLLFRGSPAGMSVOP-KNMLGCPCYROGRVSKTKTDNNNS 297
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      297 QYLRFVSTNTNGVQFQFKUL-----AGYANTYKMFPGPMGRITQNMILGSGVNAS 349
QY      298 NFTWTGASKYNLNGRESIIINFGTAMASHKODEDKFFPMGSGVMTFGKESAGASNTAL---D 354
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      350 VSAFATTMRMLEGASGVQPPQPMGMTNNGSNTYALLENMTIFNSQPANPQTATVYLEG 409
QY      355 NVMTIDDEEIKATPVPAEREGTYAVNVNROSSSTDPATGVDVAMGALPGMWQDPRVYLOG 414
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      410 NMLITTSSETOPVNRVAATNVGQAVTNQSSITPAITTYLQELVPSVMMERDVYLOG 469
QY      415 PIMAKIPTDGHFSPPLMGFGGLKNPPQLIKNTPVANPAPAEFSATKFAPIYOYST 474
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      470 PIMAKIPTGAFHPSFPMGFGGLKHPRMMLIKNTPVGN-ITFSQVUPVSSFIYOYST 528
QY      475 GQVSVIEIMELQKENSKRMPDEVQYTSYAKSANDPVVDNNGLYTERPIGTRILTRPL 534
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      529 GQVTEWEMELKENSKRMPDEIQYTNVNDPQVDFAPDSTGEYRTRPIGTRILTRPL 588

RESULT 15
US-09-533-427-4
; Sequence 4, Application US/09533427
; Patent No. 6855314
; GENERAL INFORMATION:
; APPLICANT: Chiorini, John
; APPLICANT: Kohn, Robert M.
; APPLICANT: Saefer, Brian
; APPLICANT: Davidson, Elizabeth
; APPLICANT: Zahner, Joseph
; TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
; FILE REFERENCE: 14014.0323U2
; CURRENT APPLICATION NUMBER: US/09/533,427
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

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